UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/788,793	02/27/2004	Makoto Sato	671302-2005	8148

7590 05/03/2005

THOMAS J. KOWALSKI, Esq.
c/o FROMMER LAWRENCE & HAUG LLP
745 Fifth Avenue
New York, NY 10151

EXAMINER
ROBINSON, HOPE A

ART UNIT	PAPER NUMBER
1653	

DATE MAILED: 05/03/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

PTO-90C (Rev. 10/03)

Office Action Summary	Application No.	Applicant(s)	
	10/788,793	SATO ET AL.	
	Examiner	Art Unit	
	Hope A. Robinson	1653	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *25 January 2005*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-27* is/are pending in the application.

4a) Of the above claim(s) *4-12 and 14-27* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-3 and 13* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *27 February 2004* is/are: a)☐ accepted or b)☒ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☒ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *3/17/04*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: Attachments

DETAILED ACTION

Application Status

1. Applicant's election with traverse of Group I (claims 1-3 and 13) on January 25, 2005 is acknowledged. Claims 4-12 and 14-27 are withdrawn from further consideration pursuant to 37 CFR 1.12(b), as being drawn to a non-elected invention, there being no allowable generic or linking claim.

Restriction Requirement

2. The traversal is on the grounds that Groups I-VI should be rejoined because the groups are inextricably linked (i.e. Groups I and II); there is no serious burden of search (i.e Groups I-III); and that the search is coextensive (Groups IV-VI). Essentially Applicant argues that the relatedness between Groups means that a search of one would obtain the other, thus there is no burden of search. Applicant also argues that additional cost would be incurred to the applicant and patent office with the present restriction requirement. Cost is not germane to the issue of whether or not a restriction requirement is proper, therefore, no further comments will be made on this issue by the examiner. Regarding applicant's statement that there is no burden of search, the MPEP in chapter 800 indicates that the claimed invention by acquiring a separate status in the art demonstrates search burden. Furthermore, the search of the claimed invention is not coextensive as a reference that teaches one invention would not necessarily anticipate or make obvious another invention. However, if applicant is willing to make a

statement on the record that this is the case, it will be considered. The antibody, protein, DNA and non-human animal products are patentably distinct (Inventions I-V) as outlined in the previous office action, they have different structures, functions and modes of operation. For example, although the DNA encodes the protein, the DNA can be used to make probes or primers or used in a hybridization assay. Further, the protein can be used to make antibodies or in a bioassay. The method set forth in Invention VI is not the only process that the product can be used in. Moreover, MPEP chapter 800 state that a restriction requirement is proper if the inventions are independent or distinct (related or unrelated). Therefore the restriction requirement is deemed proper and is final.

Specification

3. The specification is objected to because of the following informalities:

(a) The specification is objected to because trademarks are disclosed throughout the instant specification and not all of them are capitalized or accompanied by the generic terminology. The use of the trademarks such as FIAGS™, GENBANK™, TRITON®-X-100, TRIS®, for example, have been noted in this application (see pages 17 and 32-34). It should be capitalized wherever it appears and be accompanied by the generic terminology. Although the use of trademarks is permissible in patent applications, the proprietary nature of the marks should be respected and every effort made to prevent their use in any manner, which might adversely affect their validity as trademarks.

(b) The specification is objected to because it contains an embedded hyperlink and/or other form of browser-executable code. Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See MPEP § 608.01. See pages 14 (lines 13 and 25) and pages 15-17 for example. It is suggested that http:// is deleted.

(c) The following typographical error appears on page 41 of the instant specification, "antiboies" which should be "antibodies".

(d) The sequence notation throughout the instant specification is improper. See for example, "Seq. ID Nos. 5 and 6" on page 5 which should be "SEQ ID NOS:5 and 6".

(e) The word "of" is missing following the word "consisting" on page 6, lines 11 and 22.

(f) The specification is objected to because the claims appear on pages 42-46 of the instant specification instead of on a separate page. If applicant intends this to be text, the claim numbers should be removed.

(g) The specification is objected to because "paragraphs" are referred to throughout the specification, see for example page 6 where the following appears "(paragraph 1)"; "(paragraph 2)" etc. Applicant is reminded of the proper format of the specification below.

The following guidelines illustrate the preferred layout for the specification of a utility application. These guidelines are suggested for the applicant's use.

Arrangement of the Specification

As provided in 37 CFR 1.77(b), the specification of a utility application should include the following sections in order. Each of the lettered items should appear in

upper case, without underlining or bold type, as a section heading. If no text follows the section heading, the phrase "Not Applicable" should follow the section heading:

(a) TITLE OF THE INVENTION.
(b) CROSS-REFERENCE TO RELATED APPLICATIONS.
(c) STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT.
(d) THE NAMES OF THE PARTIES TO A JOINT RESEARCH AGREEMENT
(e) INCORPORATION-BY-REFERENCE OF MATERIAL SUBMITTED ON A COMPACT DISC (See 37 CFR 1.52(e)(5) and MPEP 608.05. Computer program listings (37 CFR 1.96(c)), "Sequence Listings" (37 CFR 1.821(c)), and tables having more than 50 pages of text are permitted to be submitted on compact discs.) or
REFERENCE TO A "MICROFICHE APPENDIX" (See MPEP § 608.05(a). "Microfiche Appendices" were accepted by the Office until March 1, 2001.)
(f) BACKGROUND OF THE INVENTION.
(1) Field of the Invention.
(2) Description of Related Art including information disclosed under 37 CFR 1.97 and 1.98.
(g) BRIEF SUMMARY OF THE INVENTION.
(h) BRIEF DESCRIPTION OF THE SEVERAL VIEWS OF THE DRAWING(S).
(i) DETAILED DESCRIPTION OF THE INVENTION.
(j) CLAIM OR CLAIMS (commencing on a separate sheet).
(k) ABSTRACT OF THE DISCLOSURE (commencing on a separate sheet).
(l) SEQUENCE LISTING (See MPEP § 2424 and 37 CFR 1.821-1.825. A "Sequence Listing" is required on paper if the application discloses a nucleotide or amino acid sequence as defined in 37 CFR 1.821(a) and if the required "Sequence Listing" is not submitted as an electronic document on compact disc).

Correction of the above and compliance with the sequence rules is required.

Drawing

4. It is noted that this application contains drawings executed in color (for example, Fig. 1), however, it does not appear that a petition to accept the drawings has been

filed. A decision on the petition will occur under separate cover once filed. Therefore, the drawings are objected to. Hence Figures such as Fig. 1 appears dark.

Information Disclosure Statement

5. The Information Disclosure Statement filed on March 17, 2004 has been received and entered. The references cited on the PTO-1449 Form have been considered by the examiner and a copy is attached to the instant Office action.

Claim Objection

6. Claims 3 and 13 is objected to because of the following informalities:

Claim 3 is objected to for the recitation of "65C" instead of "65°C".

Claim 13 is indefinite because the claim depends from a non-elected claim.

Correction of the above is required.

Claim Rejections - 35 USC ∋ 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

7. Claims 1-3 and 13 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claimed invention is directed to an isolated DNA molecule that encodes a protein that controls cell migration and cell death wherein one or several amino acids are deleted, substituted or added or wherein all or part of the sequences is present or a DNA that hybridizes to the encoding DNA under stringent conditions and the conditions provided are merely exemplary, not limiting (see claims 1-3). The claims encompass a large genus that has not been adequately described. In addition, based on the open language "comprising", the claimed fragment is unlimited, thus having an undefined structure (see claim 1 for example). Note that claim 13 is directed to a host cell the comprise the encoded protein or a part of the protein and no description is provided as to what part of the protein the host cell is capable of expressing. Therefore, the claims read on several fragments, which have not been adequately described, and there is no indication as to a conserved region or where in the sequence the modifications could occur. Furthermore, the claims encompass a sequence that is completely deleted. Therefore, the skilled artisan cannot envision the detailed chemical structure of the claimed protein fragments, thus, claims reciting said protein fragments polypeptide lacks adequate written description. Additionally, claim 3 is directed to a DNA sequence that hybridizes under stringent conditions to the claimed DNA, however, the claim provides an example of stringent conditions, which is not limiting. It is known in the prior art that

hybridization conditions can vary; therefore, the claims need to recite the actual hybridization conditions. Further, the discussion provided in the instant specification does not breathe life into the claims. Note also that claim 2 recites the language "comprising part or all of either of these sequences" and the claim does not recite any functional language, thus said protein might not be biologically active or have a different activity other than cell migration and cell death control.

The instant specification disclose that the protein controls cell migration and cell death, however, there is no demonstration of a protein that has one or several amino acids deleted retaining this function. The specification lacks adequate written description for the claimed fragments thereof, with regard to size, structure and function (i.e. is function retained or is the fragment non-functional or possess a different function). The specification fails to provide any additional representative species of the claimed genus to show that applicant was in possession of the claimed genus. A representative number of species means that the species, which are adequately described, are representative of the entire genus. The written description requirement for a claimed genus may be satisfied through sufficient description of a representative number of species by actual reduction to practice, disclosure of drawings, or by disclosure of relevant identifying characteristics, for example, structure or other physical and/or chemical properties, by functional characteristics coupled with a known or disclosed correlation between function and structure, or by a combination of such identifying characteristics, sufficient to show the applicant was in possession of the claimed genus.

Accordingly, in the absence of sufficient recitation of distinguishing identifying characteristics, the specification does not provide adequate written description of the claimed genus. The claimed genus of protein fragments could include non-functional proteins or proteins with a different function than the one described. Therefore, the genus of claimed fragments encompasses widely variant species. As such, neither the description of the structure and function of SEQ ID NOS: 2, 4 and 6, for example, controlling cell migration and cell death is sufficient to be representative of the attributes and features of the entire genus. Based on the unlimited variations contemplated one skilled in the art would at best expect a protein that is different or at worst a protein that is not functional.

Vas-Cath Inc. v. Mahurkar, 935 F.2d 1555, 1563-64, 19 USPQ2d 1111, 1117 (Fed. Cir.1991), states that "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in *possession of the invention*. The invention is, for purposes of the 'written description' inquiry, *whatever is now claimed*" (See page 1117). The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed" (See *Vas-Cath* at page 1116). The skilled artisan cannot envision the detailed chemical structure of the encompassed genus of polypeptides, and therefore, conception is not achieved until reduction to practice has occurred, regardless of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method of isolating it. The

compound itself is required. *See Fiers v. Revel, 25 USPQ2d 1601 at 1606 (CAFC 1993).*

Therefore, for all these reasons the specification lacks adequate written description, and one of skill in the art cannot reasonably conclude that the applicant had possession of the claimed invention at the time the instant application was filed.

8. Claims 1-3 and 13 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for the DNA encoding proteins set forth in SEQ ID NOS: 2, 4 and 6 that controls cell migration and cell death, does not reasonably provide enablement for any protein fragment thereof. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make the invention commensurate in scope with these claims. The enablement requirement refers to the requirement that the specification describe how to make and how to use the invention. There are many factors to be considered when determining whether there is sufficient evidence to support a determination that a disclosure does not satisfy the enablement requirement and whether any necessary experimentation is undue. These factors include, but are not limited to: Quantity of Experimentation Necessary; Amount of direction or guidance presented; Presence or absence of working examples; Nature of the Invention; State of the prior art and Relative skill of those in the art; Predictability or unpredictability of the art and Breadth of

the claims (see *In re Wands, 858 F.2d at 737, 8 USPQ2d at1404 (Fed. Cir. 1988*). The factors most relevant to the instant invention are discussed below.

The amount of experimentation required to practice the claimed invention is undue as the claims encompass an unspecified amount of protein fragments, which may not retain the ascribed function. Based on the large amount of variability contemplated said protein fragment may not have the function ascribed to SEQ ID NOS: 2, 4 and 6 (controlling cell migration and cell death), however, the claims are directed to a DNA that encodes a protein comprising an amino acid sequence wherein 1 or several amino acids are deleted, substituted or added in SEQ ID NOS: 2, 4 and 6 and the fragments encompassed are not exemplified with the ascribed function. Thus the entire sequence could be substituted or deleted as there is limitation on the amount of residues that could be deleted or substituted. Further, the claims encompass an unlimited amount of additions, therefore, based on the modifications contemplated the claimed protein could have no function or a different function. The specification does not describe properties of the claimed fragment, such as size; or demonstrate any such fragment retaining the activity of the native protein. Note also that claim 2 recites the language "part or all of either of these sequences" and the claim does not recite a functional limitation, therefore, the claimed protein once modified may not be biologically active or may not retain. Additionally, claim 13 recites "a host cell that comprises an expression system which is capable of expressing the protein...". The language "capable of " recited in the claim is not demonstrative of the claimed protein actually being expressed as the term "capable of" means that the event may not occur.

Moreover, claim 13 is directed to a host cell that is capable of expressing a part of the protein and there is no guidance provided as to what part of the protein the host cell is capable of expressing.

The instant specification does not demonstrate or provide guidance as to what the structure of the protein will be once modified or if said protein will be functional or exhibit the same properties or characteristics as the native protein. Additionally, there is no data provided demonstrative of a particular portion of the structure that must be conserved. The art recognizes Filamin A regulates cortical cell migration out of ventricular zone (Nagano et al., Nat. Cell Biol., 2002, July, vol. 4, no.7, pages 495-501). A search of the claimed sequences discloses proteins that are 69.9% or 19% identical to the claimed sequence, however, have a different function and these proteins are encompassed in the claim. For example, HYSEQ INC. disclose a protein that has 73.68% identity to SEQ ID NO:1 and SEQ ID NO:2 (DNA and the encoding the protein, respectively), however, the reference indicates that the protein is useful for treating diseases of the peripheral nervous system, such a neuropathies like Alzheimer's, Parkinson's disease, Huntington's disease, Shy-Drager Syndrome, Amyotrophic lateral sclerosis etc., therefore, the instant claims and specification needs to provide sufficient information regarding the activity to the protein to be altered in the claims. Thus, due to the large quantity of experimentation necessary to generate the infinite number of variants/fragments recited in the claims and possibly screen same for activity and the lack of guidance/direction provided in the instant specification, this is merely an invitation to the skilled artisan to use the current invention as a starting point for further

experimentation. Thus, undue experimentation would be required for a skilled artisan to make and/or use the claimed invention commensurate in scope with the claims.

Predictability of which potential changes can be tolerated in a protein's amino acid sequence and obtain the desired activity requires a knowledge of and guidance with regard to which amino acids in the protein's sequence, if any, are tolerant of modification and which are conserved (for example, expectedly intolerant to modification), and detailed knowledge of the ways in which the protein's structure relates to its function. In addition, one skilled in the art would expect any tolerance to modification for a given protein to diminish with each further and additional modification, for example, multiple substitutions. In this case, the necessary guidance has not been provided in the specification. Therefore, while it is known in the art that many amino acid substitutions are possible in any given protein, the positions within the protein's sequence where such amino acid substitutions can be made with a reasonable expectation of success are limited, as certain positions in the sequence are critical to the protein's structure/function relationship. It is also known in the art that a single nucleotide or amino acid change or mutation can destroy the function of the biomolecule in many cases. For example, various sites or regions directly involved in binding activity and in providing the correct three-dimensional spatial orientation of binding and active sites can be affected (see Wells, Biochemistry, vol. 29, pages 8509-8517, 1990). The instant specification provides no guidance/direction as to which regions of the protein would be tolerant of modifications and which would not, and it provides no working examples of any variant sequence that is encompassed by the claims. It is in no way

predictable that randomly selected mutations, such as deletions, substitutions, additions, etc., in the disclosed sequences would result in a protein having activity comparable to the one disclosed. As plural substitutions for example are introduced, their interactions with each other and their effects on the structure and function of the protein is unpredictable. The skilled artisan would recognize the high degree of unpredictability that all the fragments/variants encompassed in the claims would retain the recited function.

The state of the prior art provides evidence for the high degree of unpredictability as stated above. Seffernick et al. (J. Bacteriology, vol. 183, pages 2405-2410, 2001) disclose two polypeptides having 98% sequence identity and 99% sequence identity, differing at only 9 out of 475 amino acids (page 2407, right column, middle and page 2408, Fig. 3). The polypeptides of Seffernick et al. are identical along relatively long stretches of their respective sequences (page 2408, Fig. 3), however, these polypeptides exhibit distinct functions. The modifications exemplified in the Seffernick et al. reference is small compared to those contemplated and encompassed by the claimed invention (see page 21 of the specification and claim 3, for example). Further, Saus et al. (US PGPUB No. 2003010855A1, 2002) disclose a DNA encoding a protein that is 31.72% identical to SEQ ID NO:1, which encodes SEQ ID NO:2 of the instant application, and it is disclosed that the protein is a GIP family protein, proteins with transcription factor activity. The DNA encoding the protein of the Saus et al. reference is encompassed in the claimed limitation of 1 or several deletions, which demonstrates the unpredictability of the fragment.

The specification lacks adequate guidance/direction to enable a skilled artisan to practice the claimed invention commensurate in scope with the claims. Furthermore, while recombinant and mutagenesis techniques are known in the art, it is not routine in the art to screen large numbers of mutated proteins where the expectation of obtaining similar activity is unpredictable based on the instant disclosure. The amino acid sequence of a protein determines its structural and functional properties, and predictability of what mutations can be tolerated in a protein's sequence and result in certain activity, which is very complex, and well outside the realm of routine experimentation, because accurate predictions of a protein's function from mere sequence data are limited, therefore, the general knowledge and skill in the art is not sufficient, thus the specification needs to provide an enabling disclosure.

The working examples provided do not rectify the missing information in the instant specification pertaining to the claimed fragment/variant. The nature and properties of the claims is difficult to ascertain from the examples provided as one of skill in the art would have to engage in undue experimentation to construct the variants/fragments of the claimed invention and examine the same for function.

The specification does not provide support for the broad scope of the claims, which encompass an unspecified amount of fragments. The claims broadly read on any fragment for the given sequences (SEQ ID NOS: 2, 4 and 6). The issue in this case is the breath of the claims in light of the predictability of the art as determined by the number of working examples, the skill level artisan and the guidance presented in the instant specification and the prior art of record. This make and test position is

inconsistent with the decisions of *In re Fisher, 427 F.2d 833, 839, 166 USPQ 18, 24 (CCPA 1970)* where it is stated that "...scope of claims must bear a reasonable correlation to scope of enablement provided by the specification to persons of ordinary skill in the art...". Without sufficient guidance, determination of having the desired biological characteristics is unpredictable and the experimentation left to those skilled in the art is unnecessarily and improperly extensive and undue. See *In re Wands, 858 F.2d at 737, 8 USPQ2d at 1404 (Fed. Cir. 1988)*. Therefore, absent direction/guidance regarding whether the structure of the encoded protein can tolerate the modifications contemplated a non-functional protein may result and one of skill in the art would not be able to practice the claimed invention commensurate in scope with the claims.

Thus, for all these reasons, the specification is not considered to be enabling for one skilled in the art to make and use the claimed invention as the amount of experimentation required is undue, due to the broad scope of the claims, the lack of guidance and working examples provided in the specification and the high degree of unpredictability as evidenced by the state of the prior art, attempting to construct and test variants of the claimed invention would constitute undue experimentation. Making and testing the infinite number of possible fragments to find one that functions as described is undue experimentation. Therefore, applicants have not provided sufficient guidance to enable one of skill in the art to make and use the claimed invention in a manner that reasonably correlates with the scope of the claims, to be considered enabling.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter, which the applicant regards as his invention.

9. Claims 1-3 are rejected under 35 U.S.C. 112, second paragraph, as failing to set forth the subject matter, which applicant (s) regard as their invention.

Claim 1 is indefinite for the recitation of one or several amino acids are deleted because there is no upper limit, therefore, the entire sequence could be deleted. The dependent claims hereto are also included in this rejection as they do not rectify the deficiency.

Claim 3 is indefinite for the recitation of "e.g." in association with the hybridization conditions because this is not limiting. It is well known in the art that hybridization conditions can vary thus, if an example is provided and not the actual conditions applicant intends, the metes and bounds of the claim is unclear. The claim is also confusing, note that line three of the claim has a period following the pH and another sentence that cannot stand alone. It is suggested that the claim is amended to recite the hybridization conditions that is intended for the claimed invention and delete the period. Note also the phrase "stringent conditions" is recited twice in line two of the claim.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

10. Claims 1-3 and 13 are rejected under 35 U.S.C. 102(b) as being anticipated by Yen et al. (U.S. Patent No. 5599919, February 4, 1997), based on the broad recitation of one or several amino acids are deleted, substituted or added; a sequence comprising part or all of either of the sequences.

Yen et al. disclose a DNA encoding a protein which is 20.6% identical to the claimed sequences set forth in SEQ ID NOS: 1 and 2, therefore, which anticipates claims 1-2. In addition, the patent teaches expression in a host cell (claim 13, see column 7). As the referenced sequence has 20.6% sequence identity to the claimed sequences, the referenced DNA would hybridize to the claimed sequence. The functional property recited in the claims although not taught by the reference would be construed as an inherent property. Therefore, the limitations of the claims are met by this reference.

Conclusion

11. No claims are presently allowable.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Hope A. Robinson whose telephone number is 571-272-0957. The examiner can normally be reached on Monday-Friday.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Jon P. Weber, can be reached at (571) 272-0925. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Hope Robinson, MS HR 4/14/05

Patent Examiner

```
Qy       1875 GGCATAGAGGAGGTAGAAAGGGAAATAAACCGAGGTAGGTCGTGCAAGGGGTCTGAGTTC 1934
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GlyIleGluGluValGluArgGluIleAsnArgGlyArgSerCysLysGlySerGluPhe 620

Qy       1935 ACCTGCCCGGAAGACAATAAGATCAGAGAACTAACGCTTGAAATCGAGAGACTGAAGAAA 1994
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 ThrCysProGluAspAsnLysIleArgGluLeuThrLeuGluIleGluArgLeuLysLys 640

Qy       1995 CGGCTCCAGCAGTTGGAGGTGGTGGAGGGGGACTTGATGAAGACCGAGGACGAATATGAC 2054
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        641 ArgLeuGlnGlnLeuGluValValGluGlyAspLeuMetLysThrGluAspGluTyrAsp 660

Qy       2055 CAGTTGGAGCAGAAGTTCAGAACCGAGCAGGATAAGGCAAACTTCCTCTCCCAGCAGCTC 2114
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GlnLeuGluGlnLysPheArgThrGluGlnAspLysAlaAsnPheLeuSerGlnGlnLeu 680

Qy       2115 GAGGAAATCAAACACCAAATGGCCAAGCACAAAGCCATAGAGAAAGGGGAGGCCGTGAGC 2174
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 GluGluIleLysHisGlnMetAlaLysHisLysAlaIleGluLysGlyGluAlaValSer 700

Qy       2175 CAGGAAGCCGAACTGCGACACAGGTTTCGGCTGGAGGAGGCTAAAAGTCGTGATTTACAG 2234
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        701 GlnGluAlaGluLeuArgHisArgPheArgLeuGluGluAlaLysSerArgAspLeuGln 720

Qy       2235 GCCGAGGTGCAGGCTCTCAAGGAGAAGATCCACGAGCTGATGAACAAGGAAGACCAGCTG 2294
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AlaGluValGlnAlaLeuLysGluLysIleHisGluLeuMetAsnLysGluAspGlnLeu 740

Qy       2295 TCTCAGCTCCAAGTCGACTATTCGGTCCTTCAGCAAAGATTTATGGAAGAAGAAACTAAG 2354
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 SerGlnLeuGlnValAspTyrSerValLeuGlnGlnArgPheMetGluGluGluThrLys,760

Qy       2355 AACAAGAACATGGGGAGGGAGGTCCTCAATCTGACCAAGGAGCTAGAGCTTTCCAAGCGC 2414
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        761 AsnLysAsnMetGlyArgGluValLeuAsnLeuThrLysGluLeuGluLeuSerLysArg 780

Qy       2415 TACAGCCGAGCTCTCAGGCCGAGTGGGAACGGCCGAAGGATGGTGGACGTGCCTGTGGCC 2474
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TyrSerArgAlaLeuArgProSerGlyAsnGlyArgArgMetValAspValProValAla 800

Qy       2475 TCCACTGGGGTGCAGACCGAGGCGGTGTGCGGGGATGCTGCGGAGGAGGAGACCCCGGCT 2534
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 SerThrGlyValGlnThrGluAlaValCysGlyAspAlaAlaGluGluGluThrProAla 820

Qy       2535 GTGTTCATTCGCAAATCCTTCCAGGAGGAAAATCACATCATGAGTAATCTTCGACAGGTA 2594
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        821 ValPheIleArgLysSerPheGlnGluGluAsnHisIleMetSerAsnLeuArgGlnVal 840

Qy       2595 GGCCTGAAGAAACCCATGGAACGGTCCTCGGTCCTCGACAGGTATCCCCCAGCAGCGAAT 2654
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GlyLeuLysLysProMetGluArgSerSerValLeuAspArgTyrProProAlaAlaAsn 860

Qy       2655 GAGCTCACCATGAGGAAGTCTTGGATTCCTTGGATGAGAAAAAGAGAAAACGGTCCTTCC 2714
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GluLeuThrMetArgLysSerTrpIleProTrpMetArgLysArgGluAsnGlyProSer 880

Qy       2715 ACTCCGCAGGAGAAAGGGCCCAGGCCAAACCAGGGTGCAGGGCACCCCGGGGAGCTGGTC 2774
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        881 ThrProGlnGluLysGlyProArgProAsnGlnGlyAlaGlyHisProGlyGluLeuVal 900

Qy       2775 CTAGCACCAAAGCAGGGCCAGCCCCTACACATCCGTGTGACACCAGATCATGAGAACAGC 2834
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 LeuAlaProLysGlnGlyGlnProLeuHisIleArgValThrProAspHisGluAsnSer 920

Qy       2835 ACTGCCACCCTGGAGATCACAAGCCCCACATCTGAAGAGTTTTTCTCTAGTACCACCGTC 2894
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ThrAlaThrLeuGluIleThrSerProThrSerGluGluPhePheSerSerThrThrVal 940

Qy       2895 ATTCCTACCTTAGGCAACCAGAAACCAAGAATAACCATTATTCCATCACCCAATGTCATG 2954
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        941 IleProThrLeuGlyAsnGlnLysProArgIleThrIleIleProSerProAsnValMet 960

Qy       2955 TCGCAAAAGCCCAAAAGTGCAGATCCTACTCTCGGCCCAGAACGAGCCATGTCCCCTGTC 3014
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 SerGlnLysProLysSerAlaAspProThrLeuGlyProGluArgAlaMetSerProVal 980

Qy       3015 ACGATTACTACTATTTCCAGAGAGAAGAGCCCGGAAGGTGGAAGGAGCGCCTTTGCCGAC 3074
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         981 ThrIleThrThrIleSerArgGluLysSerProGluGlyGlyArgSerAlaPheAlaAsp 1000

Qy       3075 AGGCCTGCATCCCCCATCCAAATCATGACGGTGTCAACATCTGCAGCTCCCACTGAAATC 3134
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1001 ArgProAlaSerProIleGlnIleMetThrValSerThrSerAlaAlaProThrGluIle 1020

Qy       3135 GCTGTCTCTCCTGAATCTCAGGAAGTGCCTATGGGAAGGACTATCCTCAAAGTCACCCCG 3194
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 AlaValSerProGluSerGlnGluValProMetGlyArgThrIleLeuLysValThrPro 1040

Qy       3195 GAAAAACAAACTGTTCCAGCCCCCGTGCGGAAGTACAACTCCAATGCTAATATCATCACC 3254
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1041 GluLysGlnThrValProAlaProValArgLysTyrAsnSerAsnAlaAsnIleIleThr 1060

Qy       3255 ACGGAAGACAATAAAATTCACATTCACCTGGGTTCTCAGTTTAAGCGATCTCCTGGGCCT 3314
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1061 ThrGluAspAsnLysIleHisIleHisLeuGlySerGlnPheLysArgSerProGlyPro 1080

Qy       3315 GCCGCTGAAGGCGTGAGCCCAGTTATCACCGTCCGGCCTGTCAACGTGACAGCGGAGAAG 3374
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 AlaAlaGluGlyValSerProValIleThrValArgProValAsnValThrAlaGluLys 1100

Qy       3375 GAGGTTTCTACAGGCACAGTCCTTCGCTCTCCCAGGAACCACCTCTCTTCAAGACCCGGT 3434
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1101 GluValSerThrGlyThrValLeuArgSerProArgAsnHisLeuSerSerArgProGly 1120

Qy       3435 GCTAGCAAAGTGACCAGCACTATAACTATAACCCCGGTCACAACGTCATCCACACGAGGA 3494
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1121 AlaSerLysValThrSerThrIleThrIleThrProValThrThrSerSerThrArgGly 1140

Qy       3495 ACCCAATCAGTGTCAGGACAAGATGGGTCATCTCAGCGGCCTACCCCCACCCGCATTCCT 3554
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 ThrGlnSerValSerGlyGlnAspGlySerSerGlnArgProThrProThrArgIlePro 1160

Qy       3555 ATGTCAAAAGGTATGAAAGCTGGAAAGCCAGTAGTGGCAGCCTCAGGAGCAGGAAATCTG 3614
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1161 MetSerLysGlyMetLysAlaGlyLysProValValAlaAlaSerGlyAlaGlyAsnLeu 1180

Qy       3615 ACCAAATTCCAGCCTCGAGCTGAGACTCAGTCTATGAAAATAGAGCTGAAGAAATCTGCA 3674
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1181 ThrLysPheGlnProArgAlaGluThrGlnSerMetLysIleGluLeuLysLysSerAla 1200

Qy       3675 GCCAGCAGCACTGCCTCTCTTGGAGGGGGGAAGGGC 3710
             ||||||||||||||||||||||||||||||||||||
Db        1201 AlaSerSerThrAlaSerLeuGlyGlyGlyLysGly 1212
```

RESULT 2
AAM40016
ID AAM40016 standard; protein; 1213 AA.
XX
AC AAM40016;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 3161.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX

PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI59172.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Example 4; SEQ ID NO 3161; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 1213 AA;

Alignment Scores:

Pred. No.:	0		
Score:	5696.50	Length:	1213
Percent Similarity:	96.54%	Matches:	1134
Best Local Similarity:	93.49%	Conservative:	37
Query Match:	73.68%	Mismatches:	41
DB:	4	Indels:	1
		Gaps:	1

US-10-788-793-1 (1-4364) x AAM40016 (1-1213)

```
Qy        75 ATGAGATCACGAAATCAAGGTGGAGAAAGTTCATCTAACGGGCATGTCTCCTGCCCCAAG 134
Db         1 MetArgSerArgAsnGlnGlyGlyGluSerAlaSerAspGlyHisIleSerCysProLys 20

Qy       135 TCCTCCATCATCAGCAGTGATGGTGGTAAGGGCCCCTCAGAAGATGCA---AAAAAGAAC 191
Db        21 ProSerIleIleGlyAsnAlaGlyGluLysSerLeuSerGluAspAlaLysLysLysLys 40

Qy       192 AAGGCCAATCGGAAGGAGGAGGATGTCATGGCTTCCGGAACTATCAAAAGGCACCTCAAA 251
Db        41 LysSerAsnArgLysGluAspAspValMetAlaSerGlyThrValLysArgHisLeuLys 60

Qy       252 CCATCTGGAGAAAGTGAGAAAAAGACTAAGAAGTCTGTGGAGTTATCCAAGGAGGACCTC 311
Db        61 ThrSerGlyGluCysGluArgLysThrLysLysSerLeuGluLeuSerLysGluAspLeu 80

Qy       312 ATCCAGCTCCTGAGTATCATGGAAGGGGAGTTGCAGGCTCGAGAAGATGTCATCCACATG 371
```

```
Db        81 IleGlnLeuLeuSerIleMetGluGlyGluLeuGlnAlaArgGluAspValIleHisMet 100

Qy       372 CTGAGGACAGAGAAAACCAAGCCCGAGGTTCTGGAGGCACACTATGGATCTGCAGAACCT 431
Db       101 LeuLysThrGluLysThrLysProGluValLeuGluAlaHisTyrGlySerAlaGluPro 120

Qy       432 GAGAAAGTGCTTCGGGTCCTGCACCGAGATGCCATCCTTGCTCAAGAGAAGTCCATAGGA 491
Db       121 GluLysValLeuArgValLeuHisArgAspAlaIleLeuAlaGlnGluLysSerIleGly 140

Qy       492 GAAGACGTCTATGAGAAACCTATCTCAGAGCTGGACAGACTGGAGGAAAAGCAGAAGGAG 551
Db       141 GluAspValTyrGluLysProIleSerGluLeuAspArgLeuGluGluLysGlnLysGlu 160

Qy       552 ACGTACCGCCGCATGCTAGAGCAGCTGCTGCTGGCTGAGAAGTGTCACAGGCGCACCGTG 611
Db       161 ThrTyrArgArgMetLeuGluGlnLeuLeuLeuAlaGluLysCysHisArgArgThrVal 180

Qy       612 TACGAGCTGGAGAACGAGAAGCACAAGCACACTGACTACATGAACAAGAGCGACGACTTC 671
Db       181 TyrGluLeuGluAsnGluLysHisLysHisThrAspTyrMetAsnLysSerAspAspPhe 200

Qy       672 ACCAACCTGCTGGAGCAGGAGCGAGAGAGGTTGAAAAAGCTCCTTGAACAAGAAAAAGCT 731
Db       201 ThrAsnLeuLeuGluGlnGluArgGluArgLeuLysLysLeuLeuGluGlnGluLysAla 220

Qy       732 TACCAAGCCCGCAAAGAAAAGGAAAACGCTAAGCGGCTCAACAAACTTCGAGATGAGCTT 791
Db       221 TyrGlnAlaArgLysGluLysGluAsnAlaLysArgLeuAsnLysLeuArgAspGluLeu 240

Qy       792 GTGAAGCTCAAGTCCTTCGCCCTCATGTTGGTGGACGAGAGGCAGATGCACATCGAGCAA 851
Db       241 ValLysLeuLysSerPheAlaLeuMetLeuValAspGluArgGlnMetHisIleGluGln 260

Qy       852 CTGGGCCTGCAGAGTCAGAAAGTCCAGGACCTCACTCAGAAGCTGAGGGAGGAGGAAGAA 911
Db       261 LeuGlyLeuGlnSerGlnLysValGlnAspLeuThrGlnLysLeuArgGluGluGluGlu 280

Qy       912 AAACTCAAAGCGGTCACTTACAAATCCAAGGAAGACCGCCAGAAGCTGCTCAAGTTAGAA 971
Db       281 LysLeuLysAlaIleThrSerLysSerLysGluAspArgGlnLysLeuLeuLysLeuGlu 300

Qy       972 GTGGACTTCGAACACAAGGCCTCGAGGTTTTCCCAGGAGCACGAAGAGATGAACGCCAAA 1031
Db       301 ValAspPheGluHisLysAlaSerArgPheSerGlnGluHisGluGluMetAsnAlaLys 320

Qy      1032 TTGGCGAATCAAGAATCTCACAACCGGCAACTTCGACTCAAACTGGTTGGCTTATCGCAA 1091
Db       321 LeuAlaAsnGlnGluSerHisAsnArgGlnLeuArgLeuLysLeuValGlyLeuThrGln 340

Qy      1092 AGGATTGAGGAGCTGGAAGAGACCAATAAAAGCCTTCAGAAGGCAGAGGAAGAGCTCCAG 1151
Db       341 ArgIleGluGluLeuGluGluThrAsnLysAsnLeuGlnLysAlaGluGluGluLeuGln 360

Qy      1152 GAGCTGAGAGAGAAAATTGCCAAAGGGGAATGTGGAAACTCCAGTCTCATGGCGGAAGTG 1211
Db       361 GluLeuArgAspLysIleAlaLysGlyGluCysGlyAsnSerSerLeuMetAlaGluVal 380

Qy      1212 GAGAGTCTGCGCAAGCGCGTGCTTGAGATGGAGGGCAAGGATGAAGAGATCACGAAGACC 1271
Db       381 GluAsnLeuArgLysArgValLeuGluMetGluGlyLysAspGluGluIleThrLysThr 400

Qy      1272 GAGGCCCAGTGCCGGGAGCTGAAGAAGAAGCTCCAAGAGGAAGAACACCACAGCAAGGAA 1331
Db       401 GluSerGlnCysArgGluLeuArgLysLysLeuGlnGluGluGluHisHisSerLysGlu 420

Qy      1332 CTTAGACTAGAAGTGGAGAAGCTGCAGAAGAGGATGTCTGAGCTGGAGAAGCTGGAGGAA 1391
Db       421 LeuArgLeuGluValGluLysLeuGlnLysArgMetSerGluLeuGluLysLeuGluGlu 440

Qy      1392 GCGTTCAGCCGGAGTAAGTCGGAATGCACCCAGCTCCATCTGAACCTGGAGAACCAGAAG 1451
```

```
Db        441 AlaPheSerLysSerLysSerGluCysThrGlnLeuHisLeuAsnLeuGluLysGluLys 460

Qy       1452 AACCTAACCAAAGACCTGCTGAACGAGCTGGAGGTGGTCAAGAGTCGAGTTAAAGAACTC 1511
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        461 AsnLeuThrLysAspLeuLeuAsnGluLeuGluValValLysSerArgValLysGluLeu 480

Qy       1512 GAATGCTCCGAGAGTAGACTGGAGAAGGCCGAGTTAAGCCTCAAAGATGACCTTACAAAG 1571
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GluCysSerGluSerArgLeuGluLysAlaGluLeuSerLeuLysAspAspLeuThrLys 500

Qy       1572 CTGAAGTCCTTCACTGTGATGCTGGTGGATGAGAGGAAAAATATGATGGAGAAAATAAAG 1631
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 LeuLysSerPheThrValMetLeuValAspGluArgLysAsnMetMetGluLysIleLys 520

Qy       1632 CAAGAAGAGAGGAAAGTGGATGGGTTGAATAAAAACTTTAAGGTGGAGCAGGGAAAAGTC 1691
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        521 GlnGluGluArgLysValAspGlyLeuAsnLysAsnPheLysValGluGlnGlyLysVal 540

Qy       1692 ATGGATGTGACGGAAAAGCTAATCGAGGAAAGCAAGAAGCTTTTAAAACTCAAATCTGAA 1751
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MetAspValThrGluLysLeuIleGluGluSerLysLysLeuLeuLysLeuLysSerGlu 560

Qy       1752 ATGGAGGAAAAGGAGTACAGTCTGACAAAGGAGAGGGATGAGCTGATGGGTAAACTGAGG 1811
             |||||||||||| ||:::|||||:::|||||||||||||||:::|||||||||:::
Db        561 MetGluGluLysValTyrAsnLeuThrArgGluArgAspGluLeuIleGlyLysLeuLys 580

Qy       1812 AGCGAAGAAGAAAGGTCCTGTGAACTGAGCTGCAGTGTAGACTTACTAAAGAAGCGGCTT 1871
             ||||||||||||:::|||  ||||||||||||||||||||||||||||||||||||||||||
Db        581 SerGluGluGluLysSerSerGluLeuSerCysSerValAspLeuLeuLysLysArgLeu 600

Qy       1872 GATGGCATAGAGGAGGTAGAAAGGGAAATAAACCGAGGTAGGTCGTGCAAGGGGTCTGAG 1931
             ||||||||||||||||||||||||||||||||  ||||||||||||  ||||||||||||
Db        601 AspGlyIleGluGluValGluArgGluIleThrArgGlyArgSerArgLysGlySerGlu 620

Qy       1932 TTCACCTGCCCGGAAGACAATAAGATCAGAGAACTAACGCTTGAAATCGAGAGACTGAAG 1991
             ||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db        621 LeuThrCysProGluAspAsnLysIleLysGluLeuThrLeuGluIleGluArgLeuLys 640

Qy       1992 AAACGGCTCCAGCAGTTGGAGGTGGTGGAGGGGGACTTGATGAAGACCGAGGACGAATAT 2051
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        641 LysArgLeuGlnGlnLeuGluValValGluGlyAspLeuMetLysThrGluAspGluTyr 660

Qy       2052 GACCAGTTGGAGCAGAAGTTCAGAACCGAGCAGGATAAGGCAAACTTCCTCTCCCAGCAG 2111
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AspGlnLeuGluGlnLysPheArgThrGluGlnAspLysAlaAsnPheLeuSerGlnGln 680

Qy       2112 CTCGAGGAAATCAAACACCAAATGGCCAAGCACAAAGCCATAGAGAAAGGGGAGGCCGTG 2171
             ||||||||||||||||||||:::|||||:::|||||||||||||||||||   |||
Db        681 LeuGluGluIleLysHisGlnIleAlaLysAsnLysAlaIleGluLysGlyGluValVal 700

Qy       2172 AGCCAGGAAGCCGAACTGCGACACAGGTTTCGGCTGGAGGAGGCTAAAAGTCGTGATTTA 2231
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        701 SerGlnGluAlaGluLeuArgHisArgPheArgLeuGluGluAlaLysSerArgAspLeu 720

Qy       2232 CAGGCCGAGGTGCAGGCTCTCAAGGAGAAGATCCACGAGCTGATGAACAAGGAAGACCAG 2291
             :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 LysAlaGluValGlnAlaLeuLysGluLysIleHisGluLeuMetAsnLysGluAspGln 740

Qy       2292 CTGTCTCAGCTCCAAGTCGACTATTCGGTCCTTCAGCAAAGATTTATGGAAGAAGAAACT 2351
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 LeuSerGlnLeuGlnValAspTyrSerValLeuGlnGlnArgPheMetGluGluGluAsn 760

Qy       2352 AAGAACAAGAACATGGGGAGGGAGGTCCTCAATCTGACCAAGGAGCTAGAGCTTTCCAAG 2411
             ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||
Db        761 LysAsnLysAsnMetGlyGlnGluValLeuAsnLeuThrLysGluLeuGluLeuSerLys 780

Qy       2412 CGCTACAGCCGAGCTCTCAGGCCGAGTGGGAACGGCCGAAGGATGGTGGACGTGCCTGTG 2471
             ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db        781 ArgTyrSerArgAlaLeuArgProSerValAsnGlyArgArgMetValAspValProVal 800

Qy       2472 GCCTCCACTGGGGTGCAGACCGAGGCGGTGTGCGGGGATGCTGCGGAGGAGGAGACCCCG 2531
             ||||||||||||||||||:::||||||  |||:::|||||||||||||||||||||||||||
Db        801 ThrSerThrGlyValGlnThrAspAlaValSerGlyGluAlaAlaGluGluGluThrPro 820

Qy       2532 GCTGTGTTCATTCGCAAATCCTTCCAGGAGGAAAATCACATCATGAGTAATCTTCGACAG 2591
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        821 AlaValPheIleArgLysSerPheGlnGluGluAsnHisIleMetSerAsnLeuArgGln 840

Qy       2592 GTAGGCCTGAAGAAACCCATGGAACGGTCCTCGGTCCTCGACAGGTATCCCCCAGCAGCG 2651
             ||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||||
Db        841 ValGlyLeuLysLysProValGluArgSerSerValLeuAspArgTyrProProAlaAla 860

Qy       2652 AATGAGCTCACCATGAGGAAGTCTTGGATTCCTTGGATGAGAAAAAGAGAAAACGGTCCT 2711
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 AsnGluLeuThrMetArgLysSerTrpIleProTrpMetArgLysArgGluAsnGlyPro 880

Qy       2712 TCCACTCCGCAGGAGAAAGGGCCCAGGCCAAACCAGGGTGCAGGGCACCCCGGGGAGCTG 2771
             |||   ||||||||||||||||||  |||  ||||||||||||||:::
Db        881 SerIleThrGlnGluLysGlyProArgThrAsnSerSerProGlyHisProGlyGluVal 900

Qy       2772 GTCCTAGCACCAAAGCAGGGCCAGCCCCTACACATCCGTGTGACACCAGATCATGAGAAC 2831
             ||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ValLeuSerProLysGlnGlyGlnProLeuHisIleArgValThrProAspHisGluAsn 920

Qy       2832 AGCACTGCCACCCTGGAGATCACAAGCCCCACATCTGAAGAGTTTTTCTCTAGTACCACC 2891
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 SerThrAlaThrLeuGluIleThrSerProThrSerGluGluPhePheSerSerThrThr 940

Qy       2892 GTCATTCCTACCTTAGGCAACCAGAAACCAAGAATAACCATTATTCCATCACCCAATGTC 2951
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        941 ValIleProThrLeuGlyAsnGlnLysProArgIleThrIleIleProSerProAsnVal 960

Qy       2952 ATGTCGCAAAAGCCCAAAAGTGCAGATCCTACTCTCGGCCCAGAACGAGCCATGTCCCCT 3011
             |||  ||||||  ||||||  |||  ||||||||||||||||||||||||||||||||
Db        961 MetProGlnLysGlnLysSerGlyAspThrThrLeuGlyProGluArgAlaMetSerPro 980

Qy       3012 GTCACGATTACTACTATTTCCAGAGAGAAGAGCCCGGAAGGTGGAAGGAGCGCCTTTGCC 3071
             ||||||||||||||  ||||||||||:::||||||  ||||||  ||||||||||||||
Db        981 ValThrIleThrThrPheSerArgGluLysThrProGluSerGlyArgGlyAlaPheAla 1000

Qy       3072 GACAGGCCTGCATCCCCCATCCAAATCATGACGGTGTCAACATCTGCAGCTCCCACTGAA 3131
             |||||||||  ||||||||||||||||||||||||||||||||||||||||||||  |||
Db       1001 AspArgProThrSerProIleGlnIleMetThrValSerThrSerAlaAlaProAlaGlu 1020

Qy       3132 ATCGCTGTCTCTCCTGAATCTCAGGAAGTGCCTATGGGAAGGACTATCCTCAAAGTCACC 3191
             ||||||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||
Db       1021 IleAlaValSerProGluSerGlnGluMetProMetGlyArgThrIleLeuLysValThr 1040

Qy       3192 CCGGAAAAACAAACTGTTCCAGCCCCCGTGCGGAAGTACAACTCCAATGCTAATATCATC 3251
             ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db       1041 ProGluLysGlnThrValProThrProValArgLysTyrAsnSerAsnAlaAsnIleIle 1060

Qy       3252 ACCACGGAAGACAATAAAATTCACATTCACCTGGGTTCTCAGTTTAAGCGATCTCCTGGG 3311
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1061 ThrThrGluAspAsnLysIleHisIleHisLeuGlySerGlnPheLysArgSerProGly 1080

Qy       3312 CCTGCCGCTGAAGGCGTGAGCCCAGTTATCACCGTCCGGCCTGTCAACGTGACAGCGGAG 3371
                :::  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ThrSerGlyGluGlyValSerProValIleThrValArgProValAsnValThrAlaGlu 1100

Qy       3372 AAGGAGGTTTCTACAGGCACAGTCCTTCGCTCTCCCAGGAACCACCTCTCTTCAAGACCC 3431
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1101 LysGluValSerThrGlyThrValLeuArgSerProArgAsnHisLeuSerSerArgPro 1120

Qy       3432 GGTGCTAGCAAAGTGACCAGCACTATAACTATAACCCCGGTCACAACGTCATCCACACGA 3491
             ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||  |||
Db       1121 GlyAlaSerLysValThrSerThrIleThrIleThrProValThrThrSerSerAlaArg 1140

Qy       3492 GGAACCCAATCAGTGTCAGGACAAGATGGGTCATCTCAGCGGCCTACCCCCACCCGCATT 3551
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GlyThrGlnSerValSerGlyGlnAspGlySerSerGlnArgProThrProThrArgIle 1160

Qy       3552 CCTATGTCAAAAGGTATGAAAGCTGGAAAGCCAGTAGTGGCAGCCTCAGGAGCAGGAAAT 3611
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1161 ProMetSerLysGlyMetLysAlaGlyLysProValValAlaAlaProGlyAlaGlyAsn 1180
```

```
Qy       3612 CTGACCAAATTCCAGCCTCGAGCTGAGACTCAGTCTATGAAAATAGAGCTGAAGAAATCT 3671
             ||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||
Db       1181 LeuThrLysPheGluProArgAlaGluThrGlnSerMetLysIleGluLeuLysLysSer 1200

Qy       3672 GCAGCCAGCAGCACTGCCTCTCTTGGAGGGGGGGAAGGGC 3710
             |||||||||||||||   ||||||||||||||||||||||
Db       1201 AlaAlaSerSerThrThrSerLeuGlyGlyGlyLysGly 1213

RESULT 3
ABP97031
ID   ABP97031 standard; protein; 1213 AA.
XX
AC   ABP97031;
XX
DT   18-JUN-2003  (first entry)
XX
DE   Human L-FILIP protein SEQ ID NO:6.
XX
KW   L-FILIP; S-FILIP; filamin-interacting protein; cell migration;
KW   cell death; cytostatic; neuroprotective; immunosuppressive; cancer;
KW   tumour metastasis; transplantation therapy.
XX
OS   Homo sapiens.
XX
PN   WO2003018804-A1.
XX
PD   06-MAR-2003.
XX
PF   29-JUL-2002; 2002WO-JP007676.
XX
PR   27-AUG-2001; 2001JP-00256910.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Sato M, Nagano T;
XX
DR   WPI; 2003-268423/26.
DR   N-PSDB; ACC45356.
XX
PT   Proteins controlling cell migration and cell death and their encoded
PT   DNAs, applicable in developing drugs for treating or suppressing cancer
PT   or tumor metastasis or as regulators of cell migration for
PT   transplantation.
XX
PS   Claim 7; Page 82-88; 96pp; Japanese.
XX
CC   The present sequence represents human L-FILIP which is a filamin-
CC   interacting protein. L-FILIP has a function of controlling cell migration
CC   and cell death. L-FILIP has cytostatic, neuroprotective and
CC   immunosuppressive activities. The L-FILIP protein can be used for
CC   controlling cell migration and cell death, which is applicable in
CC   developing drugs for treating or suppressing cancer or tumour metastasis
CC   or as regulators of cell migration for transplantation therapy, and also
CC   for controlling the mobility and cell death of nerve cells, promoting
CC   decomposition of the actin-binding protein e.g. filamin-interacting
CC   protein in the treatment of preiventrilcular nodular heterotopia
XX
SQ   Sequence 1213 AA;

Alignment Scores:
Pred. No.:                0          Length:          1213
Score:                    5696.50    Matches:         1134
Percent Similarity:       96.54%     Conservative:    37
Best Local Similarity:    93.49%     Mismatches:      41
Query Match:              73.68%     Indels:          1
DB:                       6          Gaps:            1

US-10-788-793-1 (1-4364) x ABP97031 (1-1213)

Qy         75 ATGAGATCACGAAATCAAGGTGGAGAAAGTTCATCTAACGGGCATGTCTCCTGCCCCAAG 134
              ||||||||||||||||||||||||||||:::|||:::|||||:::||||||||||||
Db          1 MetArgSerArgAsnGlnGlyGlyGluSerAlaSerAspGlyHisIleSerCysProLys 20

Qy        135 TCCTCCATCATCAGCAGTGATGGTGGTAAGGGCCCCTCAGAAGATGCA---AAAAAGAAC 191
              |||||||||   :::   |||   |||   ||||||||||||   ||||||
Db         21 ProSerIleIleGlyAsnAlaGlyGluLysSerLeuSerGluAspAlaLysLysLysLys 40

Qy        192 AAGGCCAATCGGAAGGAGGAGGATGTCATGGCTTCCGGAACTATCAAAAGGCACCTCAAA 251
              |||:::|||||||||||:::|||||||||||||||||||:::|||||||||||||||||
Db         41 LysSerAsnArgLysGluAspAspValMetAlaSerGlyThrValLysArgHisLeuLys 60

Qy        252 CCATCTGGAGAAAGTGAGAAAAAGACTAAGAAGTCTGTGGAGTTATCCAAGGAGGACCTC 311
              |||||||||   |||:::|||||||||||||||:::|||||||||||||||||||||||
Db         61 ThrSerGlyGluCysGluArgLysThrLysLysSerLeuGluLeuSerLysGluAspLeu 80

Qy        312 ATCCAGCTCCTGAGTATCATGGAAGGGGAGTTGCAGGCTCGAGAAGATGTCATCCACATG 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 IleGlnLeuLeuSerIleMetGluGlyGluLeuGlnAlaArgGluAspValIleHisMet 100

Qy        372 CTGAGGACAGAGAAAACCAAGCCCGAGGTTCTGGAGGCACACTATGGATCTGCAGAACCT 431
              |||:::|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 LeuLysThrGluLysThrLysProGluValLeuGluAlaHisTyrGlySerAlaGluPro 120

Qy        432 GAGAAAGTGCTTCGGGTCCTGCACCGAGATGCCATCCTTGCTCAAGAGAAGTCCATAGGA 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GluLysValLeuArgValLeuHisArgAspAlaIleLeuAlaGlnGluLysSerIleGly 140

Qy        492 GAAGACGTCTATGAGAAACCTATCTCAGAGCTGGACAGACTGGAGGAAAAGCAGAAGGAG 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 GluAspValTyrGluLysProIleSerGluLeuAspArgLeuGluGluLysGlnLysGlu 160

Qy        552 ACGTACCGCCGCATGCTAGAGCAGCTGCTGCTGGCTGAGAAGTGTCACAGGCGCACCGTG 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 ThrTyrArgArgMetLeuGluGlnLeuLeuLeuAlaGluLysCysHisArgArgThrVal 180

Qy        612 TACGAGCTGGAGAACGAGAAGCACAAGCACACTGACTACATGAACAAGAGCGACGACTTC 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TyrGluLeuGluAsnGluLysHisLysHisThrAspTyrMetAsnLysSerAspAspPhe 200

Qy        672 ACCAACCTGCTGGAGCAGGAGCGAGAGAGGTTGAAAAAGCTCCTTGAACAAGAAAAAGCT 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ThrAsnLeuLeuGluGlnGluArgGluArgLeuLysLysLeuLeuGluGlnGluLysAla 220

Qy        732 TACCAAGCCCGCAAAGAAAAGGAAAACGCTAAGCGGCTCAACAAACTTCGAGATGAGCTT 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 TyrGlnAlaArgLysGluLysGluAsnAlaLysArgLeuAsnLysLeuArgAspGluLeu 240

Qy        792 GTGAAGCTCAAGTCCTTCGCCCTCATGTTGGTGGACGAGAGGCAGATGCACATCGAGCAA 851
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ValLysLeuLysSerPheAlaLeuMetLeuValAspGluArgGlnMetHisIleGluGln 260

Qy        852 CTGGGCCTGCAGAGTCAGAAAGTCCAGGACCTCACTCAGAAGCTGAGGGAGGAGGAAGAA 911
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 LeuGlyLeuGlnSerGlnLysValGlnAspLeuThrGlnLysLeuArgGluGluGluGlu 280

Qy        912 AAACTCAAAGCGGTCACTTACAAATCCAAGGAAGACCGCCAGAAGCTGCTCAAGTTAGAA 971
              ||||||||||||:::|||   ||||||||||||||||||||||||||||||||||||||
Db        281 LysLeuLysAlaIleThrSerLysSerLysGluAspArgGlnLysLeuLeuLysLeuGlu 300

Qy        972 GTGGACTTCGAACACAAGGCCTCGAGGTTTTCCCAGGAGCACGAAGAGATGAACGCCAAA 1031
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ValAspPheGluHisLysAlaSerArgPheSerGlnGluHisGluGluMetAsnAlaLys 320

Qy       1032 TTGGCGAATCAAGAATCTCACAACCGGCAACTTCGACTCAAACTGGTTGGCTTATCGCAA 1091
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db        321 LeuAlaAsnGlnGluSerHisAsnArgGlnLeuArgLeuLysLeuValGlyLeuThrGln 340

Qy       1092 AGGATTGAGGAGCTGGAAGAGACCAATAAAAGCCTTCAGAAGGCAGAGGAAGAGCTCCAG 1151
              ||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||||
Db        341 ArgIleGluGluLeuGluGluThrAsnLysAsnLeuGlnLysAlaGluGluGluLeuGln 360

Qy       1152 GAGCTGAGAGAGAAAATTGCCAAAGGGGAATGTGGAAACTCCAGTCTCATGGCGGAAGTG 1211
              |||||||||:::||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GluLeuArgAspLysIleAlaLysGlyGluCysGlyAsnSerSerLeuMetAlaGluVal 380

Qy       1212 GAGAGTCTGCGCAAGCGCGTGCTTGAGATGGAGGGCAAGGATGAAGAGATCACGAAGACC 1271
```

```
Qy       2409 AAGCGCTACAGCCGAGCTCTCAGGCCGAGTGGGAACGGCCGAAGGATGGTGGACGTGCCT 2468
Db        681 LysArgTyrSerArgAlaLeuArgProSerValAsnGlyArgArgMetValAspValPro 700

Qy       2469 GTGGCCTCCACTGGGGTGCAGACCGAGGCGGTGTGCGGGGATGCTGCGGAGGAGGAGACC 2528
Db        701 ValThrSerThrGlyValGlnThrAspAlaValSerGlyGluAlaAlaGluGluGluThr 720

Qy       2529 CCGGCTGTGTTCATTCGCAAATCCTTCCAGGAGGAAAAATCACATCATGAGTAATCTTCGA 2588
Db        721 ProAlaValPheIleArgLysSerPheGlnGluGluAsnHisIleMetSerAsnLeuArg 740

Qy       2589 CAGGTAGGCCTGAAGAAACCCATGGAACGGTCCTCGGTCCTCGACAGGTATCCCCCAGCA 2648
Db        741 GlnValGlyLeuLysLysProValGluArgSerSerValLeuAspArgTyrProProAla 760

Qy       2649 GCGAATGAGCTCACCATGAGGAAGTCTTGGATTCCTTGGATGAGAAAAAGAGAAAACGGT 2708
Db        761 AlaAsnGluLeuThrMetArgLysSerTrpIleProTrpMetArgLysArgGluAsnGly 780

Qy       2709 CCTTCCACTCCGCAGGAGAAAGGGCCCAGGCCAAACCAGGGTGCAGGGCACCCCGGGGAG 2768
Db        781 ProSerIleThrGlnGluLysGlyProArgThrAsnSerSerProGlyHisProGlyGlu 800

Qy       2769 CTGGTCCTAGCACCAAAGCAGGGCCAGCCCCTACACATCCGTGTGACACCAGATCATGAG 2828
Db        801 ValValLeuSerProLysGlnGlyGlnProLeuHisIleArgValThrProAspHisGlu 820

Qy       2829 AACAGCACTGCCACCCTGGAGATCACAAGCCCCACATCTGAAGAGTTTTTCTCTAGTACC 2888
Db        821 AsnSerThrAlaThrLeuGluIleThrSerProThrSerGluGluPhePheSerSerThr 840

Qy       2889 ACCGTCATTCCTACCTTAGGCAACCAGAAACCAAGAATAACCATTATTCCATCACCCAAT 2948
Db        841 ThrValIleProThrLeuGlyAsnGlnLysProArgIleThrIleIleProSerProAsn 860

Qy       2949 GTCATGTCGCAAAAGCCCAAAAGTGCAGATCCTACTCTCGGCCCAGAACGAGCCATGTCC 3008
Db        861 ValMetProGlnLysGlnLysSerGlyAspThrThrLeuGlyProGluArgAlaMetSer 880

Qy       3009 CCTGTCACGATTACTACTATTTCCAGAGAGAAGAGCCCGGAAGGTGGAAGGAGCGCCTTT 3068
Db        881 ProValThrIleThrThrPheSerArgGluLysThrProGluSerGlyArgGlyAlaPhe 900

Qy       3069 GCCGACAGGCCTGCATCCCCCATCCAAATCATGACGGTGTCAACATCTGCAGCTCCCACT 3128
Db        901 AlaAspArgProThrSerProIleGlnIleMetThrValSerThrSerAlaAlaProAla 920

Qy       3129 GAAATCGCTGTCTCTCCTGAATCTCAGGAAGTGCCTATGGGAAGGACTATCCTCAAAGTC 3188
Db        921 GluIleAlaValSerProGluSerGlnGluMetProMetGlyArgThrIleLeuLysVal 940

Qy       3189 ACCCCGGAAAAACAAACTGTTCCAGCCCCCGTGCGGAAGTACAACTCCAATGCTAATATC 3248
Db        941 ThrProGluLysGlnThrValProThrProValArgLysTyrAsnSerAsnAlaAsnIle 960

Qy       3249 ATCACCACGGAAGACAATAAAATTCACATTCACCTGGGTTCTCAGTTTAAGCGATCTCCT 3308
Db        961 IleThrThrGluAspAsnLysIleHisIleHisLeuGlySerGlnPheLysArgSerPro 980

Qy       3309 GGGCCTGCCGCTGAAGGCGTGAGCCCAGTTATCACCGTCCGGCCTGTCAACGTGACAGCG 3368
Db        981 GlyThrSerGlyGluGlyValSerProValIleThrValArgProValAsnValThrAla 1000

Qy       3369 GAGAAGGAGGTTTCTACAGGCACAGTCCTTCGCTCTCCCAGGAACCACCTCTCTTCAAGA 3428
Db       1001 GluLysGluValSerThrGlyThrValLeuArgSerProArgAsnHisLeuSerSerArg 1020

Qy       3429 CCCGGTGCTAGCAAAGTGACCAGCACTATAACTATAACCCCGGTCACAACGTCATCCACA 3488
Db       1021 ProGlyAlaSerLysValThrSerThrIleThrIleThrProValThrThrSerSerAla 1040
```

```
Qy       3489 CGAGGAACCCAATCAGTGTCAGGACAAGATGGGTCATCTCAGCGGCCTACCCCCACCCGC 3548
Db       1041 ArgGlyThrGlnSerValSerGlyGlnAspGlySerSerGlnArgProThrProThrArg 1060

Qy       3549 ATTCCTATGTCAAAAGGTATGAAAGCTGGAAAGCCAGTAGTGGCAGCCTCAGGAGCAGGA 3608
Db       1061 IleProMetSerLysGlyMetLysAlaGlyLysProValValAlaAlaProGlyAlaGly 1080

Qy       3609 AATCTGACCAAATTCCAGCCTCGAGCTGAGACTCAGTCTATGAAAATAGAGCTGAAGAAA 3668
Db       1081 AsnLeuThrLysPheGluProArgAlaGluThrGlnSerMetLysIleGluLeuLysLys 1100

Qy       3669 TCTGCAGCCAGCAGCACTGCCTCTCTTGGAGGGGGGAAGGGC 3710
Db       1101 SerAlaAlaSerSerThrThrSerLeuGlyGlyGlyLysGly 1114
```

RESULT 2
US-10-309-851-14
; Sequence 14, Application US/10309851
; Publication No. US20030108554A1
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; APPLICANT: Revert-Ros, Francisco
; TITLE OF INVENTION: GIPs, a Family of Polypeptides with Transcription Factor Activity
; TITLE OF INVENTION: Interact with Goodpasture Antigen Binding Protein
; FILE REFERENCE: 98,723-F-US
; CURRENT APPLICATION NUMBER: US/10/309,851
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 1133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-851-14

Alignment Scores:

Pred. No.:	1.93e-139	Length:	1133
Score:	2452.50	Matches:	542
Percent Similarity:	64.40%	Conservative:	214
Best Local Similarity:	46.17%	Mismatches:	337
Query Match:	31.72%	Indels:	81
DB:	14	Gaps:	19

US-10-788-793-1 (1-4364) x US-10-309-851-14 (1-1133)

```
Qy         75 ATGAGATCACGAAATCAAGGTGGAGAAAGTTCATCTAACGGGCATGTCTCCTGCCCCAAG 134
Db          1 MetArgSerArg------GlySerAspThrGluGlySerAlaGlnLysLysPheProArg 18

Qy        135 TCCTCCATCATCAGCAGTGATGGTGGTAAGGGCCCCTCAGAAGATGCAAAAAAGAACAAG 194
Db         19 HisThr----------------------LysGlyHisSerPheGlnGlyProLysAsnMet 31

Qy        195 GCCAATCGGAAGGAGGAG---GATGTCATGGCTTCCGGAACTATCAAAAGGCACCTCAAA 251
Db         32 LysHisArgGlnGlnAspLysAspSerProSerGluSerAspVal---------IleLeu 48

Qy        252 CCATCTGGAGAAAGTGAGAAA-----------AAGACTAAGAAGTCTGTGGAGTTATCC 299
Db         49 ProCysProLysAlaGluLysProHisSerGlyAsnGlyHisGlnAlaGluAspLeuSer 68

Qy        300 AAGGAGGACCTCATCCAGCTCCTGAGTATCATGGAAGGGGAGTTGCAGGCTCGAGAAGAT 359
Db         69 ArgAspAspLeuLeuPheLeuLeuSerIleLeuGluGlyGluLeuGlnAlaArgAspGlu 88

Qy        360 GTCATCCACATGCTGAGGACAGAGAAAACCAAGCCCGAGGTTCTGGAGGCACACTATGGA 419
Db         89 ValIleGlyIleLeuLysAlaGluLysMetAspLeuAlaLeuLeuGluAlaGlnTyrGly 108

Qy        420 TCTGCAGAACCTGAGAAAGTGCTTCGGGTCCTGCACCGAGATGCCATCCTTGCTCAAGAG 479
Db        109 PheValThrProLysLysValLeuGluAlaLeuGlnArgAspAlaPheGlnAlaLysSer 128
```

```
Qy   480 AAGTCCATAGGAGAAGACGTCTATGAGAAACCTATCTCAGAGCTGGACAGACTGGAGGAA 539
Db   129 ThrProTrpGlnGluAspIleTyrGluLysProMetAsnGluLeuAspLysValValGlu 148
Qy   540 AAGCAGAAGGAGACGTACCGCCGCATGCTAGAGCAGCTGCTGCTGGCTGAGAAGTGTCAC 599
Db   149 LysHisLysGluSerTyrArgArgIleLeuGlyGlnLeuLeuValAlaGluLysSerHis 168
Qy   600 AGGCGCACCGTGTACGAGCTGGAGAACGAGAAGCACAAGCACACTGACTACATGAACAAG 659
Db   169 ArgGlnThrIleLeuGluLeuGluGluGluLysArgLysHisLysGluTyrMetGluLys 188
Qy   660 AGCGACGACTTCACCAACCTGCTGGAGCAGGAGCGAGAGAGGTTGAAAAAGCTCCTTGAA 719
Db   189 SerAspGluPheIleCysLeuLeuGluGlnGluCysGluArgLeuLysLysLeuIleAsp 208
Qy   720 CAAGAAAAAGCTTACCAAGCCCGCAAAGAAAAGGAAAACGCTAAGCGGCTCAACAAACTT 779
Db   209 GlnGluIleLysSerGlnGluGluLysGluGlnGluLysGluLysArgValThrThrLeu 228
Qy   780 CGAGATGAGCTTGTGAAGCTCAAGTCCTTCGCCCTCATGTTGGTGGACGAGAGGCAGATG 839
Db   229 LysGluGluLeuThrLysLeuLysSerPheAlaLeuMetValValAspGluGlnGlnArg 248
Qy   840 CACATCGAGCAACTGGGCCTGCAGAGTCAGAAAGTCCAGGACCTCACTCAGAAGCTGAGG 899
Db   249 LeuThrAlaGlnLeuThrLeuGlnArgGlnLysIleGlnGluLeuThrThrAsnAlaLys 268
Qy   900 GAGGAGGAAGAAAAACTCAAAGCGGTCACTTACAAATCCAAGGAAGACCGCCAGAAGCTG 959
Db   269 GluThrHisThrLysLeuAlaLeuAlaGluAlaArgValGlnGluGluGluGlnLysAla 288
Qy   960 CTCAAGTTAGAAGTGGACTTCGAACACAAGGCCTCGAGGTTTTCCCAGGAGCACGAAGAG 1019
Db   289 ThrArgLeuGluLysGluLeuGlnThrGlnThrThrLysPheHisGlnAspGlnAspThr 308
Qy  1020 ATGAACGCCAAATTGGCGAATCAAGAATCTCACAACCGGCAACTTCGACTCAAACTGGTT 1079
Db   309 IleMetAlaLysLeuThrAsnGluAspSerGlnAsnArgGlnLeuGlnGlnLysLeuAla 328
Qy  1080 GGCTTATCGCAAAGGATTGAGGAGCTGGAAGAGACCAATAAAAGCCTTCAGAAGGCAGAG 1139
Db   329 AlaLeuSerArgGlnIleAspGluLeuGluGluThrAsnArgSerLeuArgLysAlaGlu 348
Qy  1140 GAAGAGCTCCAGGAGCTGAGAGAGAAAATTGCCAAAGGGGAATGTGGAAACTCCAGTCTC 1199
Db   349 GluGluLeuGlnAspIleLysGluLysIleSerLysGlyGluTyrGlyAsnAlaGlyIle 368
Qy  1200 ATGGCGGAAGTGGAGAGTCTGCGCAAGCGCGTGCTTGAGATGGAGGGCAAGGATGAAGAG 1259
Db   369 MetAlaGluValGluGluLeuArgLysArgValLeuAspMetGluGlyLysAspGluGlu 388
Qy  1260 ATCACGAAGACCGAGGCCCAGTGCCGGGAGCTGAAGAAGAAGCTCCAAGAGGAAGAACAC 1319
Db   389 LeuIleLysMetGluGluGlnCysArgAspLeuAsnLysArgLeuGluArgGluThrLeu 408
Qy  1320 CACAGCAAGGAACTTAGACTAGAAGTGGAGAAGCTGCAGAAGAGGATGTCTGAGCTGGAG 1379
Db   409 GlnSerLysAspPheLysLeuGluValGluLysLeuSerLysArgIleMetAlaLeuGlu 428
Qy  1380 AAGCTGGAGGAAGCGTTCAGCCGGAGTAAGTCGGAATGCACCCAGCTCCATCTGAACCTG 1439
Db   429 LysLeuGluAspAlaPheAsnLysSerLysGlnGluCysTyrSerLeuLysCysAsnLeu 448
Qy  1440 GAGAAGGAGAAGAACCTAACCAAAGACCTGCTGAACGAGCTGGAGGTGGTCAAGAGTCGA 1499
Db   449 GluLysGluArgMetThrThrLysGlnLeuSerGlnGluLeuGluSerLeuLysValArg 468
Qy  1500 GTTAAAGAACTCGAATGCTCCGAGAGTAGACTGGAGAAGGCCGAGTTAAGCCTCAAAGAT 1559
Db   469 IleLysGluLeuGluAlaIleGluSerArgLeuGluLysThrGluPheThrLeuLysGlu 488

Qy  1560 GACCTTACAAAGCTGAAGTCCTTCACTGTGATGCTGGTGGATGAGAGGAAAAATATGATG 1619
Db   489 AspLeuThrLysLeuLysThrLeuThrValMetPheValAspGluArgLysThrMetSer 508
Qy  1620 GAGAAAATAAAGCAAGAAGAGAGGAAAGTGGATGGGTTGAATAAAAACTTTAAGGTGGAG 1679
Db   509 GluLysLeuLysLysThrGluAspLysLeuGlnAlaAlaSerSerGlnLeuGlnValGlu 528
Qy  1680 CAGGGAAAAGTCATGGATGTGACGGAAAAGCTAATCGAGGAAAGCAAGAAGCTTTTAAAA 1739
Db   529 GlnAsnLysValThrThrValThrGluLysLeuIleGluGluThrLysArgAlaLeuLys 548
Qy  1740 CTCAAATCTGAAATGGAGGAAAAGGAGTACAGTCTGACAAAGGAGAGGGATGAGCTGATG 1799
Db   549 SerLysThrAspValGluGluLysMetTyrSerValThrLysGluArgAspAspLeuLys 568
Qy  1800 GGTAAACTGAGGAGCGAAGAAGAAAGGTCCTGTGAACTGAGCTGCAGTGTAGACTTACTA 1859
Db   569 AsnLysLeuLysAlaGluGluGluLysGlyAsnAspLeuLeuSerArgValAsnMetLeu 588
Qy  1860 AAGAAGCGGCTTGATGGCATAGAGGAGGTAGAAAGGGAAATAAACCGAGGTAGG------ 1913
Db   589 LysAsnArgLeuGlnSerLeuGluAlaIleGluLysAspPheLeuLysAsnLysLeuAsn 608
Qy  1914 ------TCGTGCAAGGGGTCTGAGTTCACCTGCCCGGAAGACAATAAGATCAGAGAACTA 1967
Db   609 GlnAspSerGlyLysSerThrThrAlaLeuHisGlnGluAsnAsnLysIleLysGluLeu 628
Qy  1968 ACGCTTGAAATCGAGAGACTGAAGAAACGGCTCCAGCAGTTGGAGGTGGTGGAGGGGGAC 2027
Db   629 SerGlnGluValGluArgLeuLysLeuLysLeuLysAspMetLysAlaIleGluAspAsp 648
Qy  2028 TTGATGAAGACCGAGGACGAATATGACCAGTTGGAGCAGAAGTTCAGAACCGAGCAGGAT 2087
Db   649 LeuMetLysThrGluAspGluTyrGluThrLeuGluArgArgTyrAlaAsnGluArgAsp 668
Qy  2088 AAGGCAAACTTCCTCTCCCAGCAGCTCGAGGAAATCAAACACCAAATGGCCAAGCACAAA 2147
Db   669 LysAlaGlnPheLeuSerLysGluLeuGluHisValLysMetGluLeuAlaLysTyrLys 688
Qy  2148 GCCATAGAGAAAGGGGAGGCCGTGAGCCAGGAAGCCGAACTGCGACACAGGTTTCGGCTG 2207
Db   689 LeuAlaGluLysThrGlu---ThrSerHisGluGlnTrpLeuPheLysArgLeuGlnGlu 707
Qy  2208 GAGGAGGCTAAAAGTCGTGATTTACAGGCCGAGGTGCAGGCTCTCAAGGAGAAGATCCAC 2267
Db   708 GluGluAlaLysSerGlyHisLeuSerArgGluValAspAlaLeuLysGluLysIleHis 727
Qy  2268 GAGCTGATGAACAAGGAAGACCAGCTGTCTCAGCTCCAAGTCGACTATTCGGTCCTTCAG 2327
Db   728 GluTyrMetAlaThrGluAspLeuIleCysHisLeuGlnGlyAspHisSerValLeuGln 747
Qy  2328 CAAAGATTTATGGAAGAAGAAACTAAGAACAAGAACATGGGGAGGGAGGTCCTCAATCTG 2387
Db   748 LysLysLeuAsnGlnGlnGluAsnArgAsnArgAspLeuGlyArgGluIleGluAsnLeu 767
Qy  2388 ACCAAGGAGCTAGAGCTTTCCAAGCGCTACAGCCGAGCTCTCAGGCCGAGTGGGAACGGC 2447
Db   768 ThrLysGluLeuGluArgTyrArgHisPheSerLysSerLeuArgProSerLeuAsnGly 787
Qy  2448 CGAAGGATGGTGGACGTGCCTGTGGCCTCCACTGGGGTGCAGACCGAGGCGGTGTGCGGG 2507
Db   788 ArgArgIleSerAspProGlnValPheSerLysGluValGlnThrGluAlaVal------ 805
Qy  2508 GATGCTGCGGAGGAGGAGACCCCG----------GCTGTG 2537
Db   806 ---------AspAsnGluProProAspTyrLysSerLeuIleProLeuGluArgAlaVal 822
Qy  2538 TTCATTCGCAAATCCTTCCAGGAG---GAAAATCACATCATGAGTAATCTTCGACAGGTA 2594
Db   823 IleAsnGlyGlnLeuTyrGluGluSerGluAsnGlnAsp---------- 835
Qy  2595 GGCCTGAAGAAACCCATGGAACGGTCCTCGGTCCTC----------GACAGGTAT 2639
```

```
Db        836 ------GluAspProAsnAspGluGlySerValLeuSerPheLysCysSerGlnSerThr 853

Qy       2640 CCCCCAGCAGCGAATGAGCTCACCATGAGGAAGTCTTGGATTCCTTGGATGAGAAAAAGA 2699

Db        854 ProCysProValAsn------------ArgLysLeuTrpIleProTrpMetLysSerLys 869

Qy       2700 GAA------------AACGGTCCTTCCACTCCGCAGGAGAAAGGGCCCAGGCCAAACCAG 2747

Db        870 GluGlyHisLeuGlnAsnGly--------------LysMetGlnThrLysProAsnAla 884

Qy       2748 GGTGCAGGGCACCCCGGGGAGCTGGTCCTAGCACCAAAGCAGGGCCAGCCCCTACACATC 2807

Db        885 AsnPheValGlnProGlyAspLeuValLeuSerHisThrProGlyGlnProLeuHisIle 904

Qy       2808 CGTGTGACACCAGATCATGAGAACAGCACTGCCACCCTGGAGATCACAAGCCCCACATCT 2867

Db        905 LysValThrProAspHisValGlnAsnThrAlaThrLeuGluIleThrSerProThrThr 924

Qy       2868 GAA------GAGTTTTTCTCTAGTACCACCGTCATTCCTACCTTAGGCAACCAGAAACCA 2921

Db        925 GluSerProHisSerTyrThrSerThrAlaValIleProAsnCysGlyThrProLysGln 944

Qy       2922 AGAATAACCATTATTCCATCACCCAATGTCATGTCGCAAAAGCCCAAA---AGTGCAGAT 2978

Db        945 ArgIleThrIleLeuGlnAsnAlaSerIleThrProValLysSerLysThrSerThrGlu 964

Qy       2979 CCTACTCTCGGCCCAGAACGAGCCATGTCCCCTGTCACGATTACTACTATTTCCAGAGAG 3038

Db        965 AspLeuMetAsnLeuGluGlnGlyMetSerProIleThrMetAlaThrPheAlaArgAla 984

Qy       3039 AAGAGCCCGGAAGGTGGAAGGAGCGCCTTTGCCGACAGGCCTGCATCCCCCATCCAAATC 3098

Db        985 GlnThrProGluSerCysGlySerLeuThrProGluArgThrMetSerProIleGlnVal 1004

Qy       3099 ATGACGGTGTCAACATCTGCAGCTCCCACTGAAATCGCTGTCTCTCCTGAATCTCAGGAA 3158

Db       1005 LeuAlaValThrGlySerAlaSerSerProGluGlnGlyArgSerProGluProThrGlu 1024

Qy       3159 GTGCCTATGGGAAGGACTATCCTCAAAGTCACCCCGGAAAAACAAACTGTTCCAGCCCCC 3218

Db       1025 IleSerAlaLysHisAlaIlePheArgValSerProAspArgGlnSerSerTrpGlnPhe 1044

Qy       3219 GTGCGGAAGTACAACTCCAATGCTAATATCATCACCACGGAAGACAATAAAATTCACATT 3278

Db       1045 GlnArgSerAsnSerAsnSerSerSerValIleThrThrGluAspAsnLysIleHisIle 1064

Qy       3279 CACCTGGGTTCTCAGTTTAAGCGATCTCCTGGGCCTGCCGCTGAAGGCGTGAGCCCAGTT 3338

Db       1065 HisLeuGlySerProTyrMetGlnAla---------ValAlaSerProValArgProAla 1081

Qy       3339 ATCACCGTCCGGCCTGTCAACGTGACAGCGGAGAAGGAGGTTTCTACAGGCACAGTCCTT 3398

Db       1082 SerProSerAlaProLeuGlnAspAsnArgThrGlnGlyLeuIleAsnGlyAlaLeuAsn 1101

Qy       3399 CGCTCTCCCAGGAACCACCTCTCTTCAAGACCCGGTGCTAGCAAAGTGACCAGCACTATA 3458

Db       1102 LysThr-----------------------------ThrAsnLysValThrSerSerIle 1111

Qy       3459 ACTATAACCCCGGTCACAACGTCATCCACACGAGGAACCCAA 3500

Db       1112 ThrIleThrProThrAlaThrProLeuProArgGlnSerGln 1125

RESULT 3
US-10-309-851-16
; Sequence 16, Application US/10309851
; Publication No. US20030108554A1
; GENERAL INFORMATION:
;  APPLICANT: Saus, Juan
;  APPLICANT:  Revert-Ros, Francisco
;  TITLE OF INVENTION: GIPs, a Family of Polypeptides with Transcription Factor Activity
;  TITLE OF INVENTION:  Interact with Goodpasture Antigen Binding Protein
;  FILE REFERENCE: 98,723-F-US
;  CURRENT APPLICATION NUMBER: US/10/309,851
;  CURRENT FILING DATE:  2002-12-04
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 1133
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-851-16

Alignment Scores:
Pred. No.:                  5.87e-139     Length:          1133
Score:                      2444.50       Matches:          541
Percent Similarity:         64.31%        Conservative:     214
Best Local Similarity:      46.08%        Mismatches:       338
Query Match:                31.62%        Indels:            81
DB:                         14            Gaps:              19

US-10-788-793-1 (1-4364) x US-10-309-851-16 (1-1133)

Qy         75 ATGAGATCACGAAATCAAGGTGGAGAAAGTTCATCTAACGGGCATGTCTCCTGCCCCAAG 134

Db          1 MetArgSerArg------GlySerAspThrGluGlySerAlaGlnLysLysPheProArg 18

Qy        135 TCCTCCATCATCAGCAGTGATGGTGGTAAGGGCCCCTCAGAAGATGCAAAAAAGAACAAG 194

Db         19 HisThr--------------------LysGlyHisSerPheGlnGlyProLysAsnMet 31

Qy        195 GCCAATCGGAAGGAGGAG---GATGTCATGGCTTCCGGAACTATCAAAAGGCACCTCAAA 251

Db         32 LysHisArgGlnGlnAspLysAspSerProSerGluSerAspVal---------IleLeu 48

Qy        252 CCATCTGGAGAAAGTGAGAAA------------AAGACTAAGAAGTCTGTGGAGTTATCC 299

Db         49 ProCysProLysAlaGluLysProHisSerGlyAsnGlyHisGlnAlaGluAspLeuSer 68

Qy        300 AAGGAGGACCTCATCCAGCTCCTGAGTATCATGGAAGGGGAGTTGCAGGCTCGAGAAGAT 359

Db         69 ArgAspAspLeuLeuPheLeuLeuSerIleLeuGluGlyGluLeuGlnAlaArgAspGlu 88

Qy        360 GTCATCCACATGCTGAGGACAGAGAAAACCAAGCCCGAGGTTCTGGAGGCACACTATGGA 419

Db         89 ValIleGlyIleLeuLysAlaGluLysMetAspLeuAlaLeuLeuGluAlaGlnTyrGly 108

Qy        420 TCTGCAGAACCTGAGAAAGTGCTTCGGGTCCTGCACCGAGATGCCATCCTTGCTCAAGAG 479

Db        109 PheValThrProLysLysValLeuGluAlaLeuGlnArgAspAlaPheGlnAlaLysSer 128

Qy        480 AAGTCCATAGGAGAAGACGTCTATGAGAAACCTATCTCAGAGCTGGACAGACTGGAGGAA 539

Db        129 ThrProTrpGlnGluAspIleTyrGluLysProMetAsnGluLeuAspLysValValGlu 148

Qy        540 AAGCAGAAGGAGACGTACCGCCGCATGCTAGAGCAGCTGCTGCTGGCTGAGAAGTGTCAC 599

Db        149 LysHisLysGluSerTyrArgArgIleLeuGlyGlnLeuLeuValAlaGluLysSerArg 168

Qy        600 AGGCGCACCGTGTACGAGCTGGAGAACGAGAAGCACAAGCACACTGACTACATGAACAAG 659

Db        169 ArgGlnThrIleLeuGluLeuGluGluGluLysArgLysHisLysGluTyrMetGluLys 188

Qy        660 AGCGACGACTTCACCAACCTGCTGGAGCAGGAGCGAGAGAGGTTGAAAAAGCTCCTTGAA 719

Db        189 SerAspGluPheIleCysLeuLeuGluGlnGluCysGluArgLeuLysLysLeuIleAsp 208

Qy        720 CAAGAAAAAGCTTACCAAGCCCGCAAAGAAAAGGAAAACGCTAAGCGGCTCAACAAACTT 779

Db        209 GlnGluIleLysSerGlnGluGluLysGluGlnGluGluLysArgValThrThrLeu 228

Qy        780 CGAGATGAGCTTGTGAAGCTCAAGTCCTTCGCCCTCATGTTGGTGGACGAGAGGCAGATG 839

Db        229 LysGluGluLeuThrLysLeuLysSerPheAlaLeuMetValValAspGluGlnGlnArg 248

Qy        840 CACATCGAGCAACTGGGCCTGCAGAGTCAGAAAGTCCAGGACCTCACTCAGAAGCTGAGG 899
```

```
Db       1964 GluLeuGluLeuThrLysMetAspLysMetSerPheValGluLysValAsnLysMetThr 1983
Qy       2172 AGCCAGGAAGCCGAACTGCGACACAGGTTTCGGCTGGAGGAGGCTAAAAGTCGTGATTTA 2231
Db       1984 AlaLysGluThrGluLeuGlnArgGluMetHisGluMetAlaGlnLysThrAlaGluLeu 2003
Qy       2232 CAGGCCGAGGTGCAGGCTCTCAAGGAGAAG----------------------ATCCAC 2267
Db       2004 GlnGluGluLeuSerGlyGluLysAsnArgLeuAlaGlyGluLeuGlnLeuLeuGlu 2023
Qy       2268 GAGCTGATGAACAAGGAAGACCAGCTGTCTCAGCTCCAAGTCGACTATTCGGTCCTTCAG 2327
Db       2024 GluIleLysSerSerLysAspGlnLeuLysGluLeuThrLeuGluAsnSerGluLeuLys 2043
Qy       2328 CAAAGATTT-----------ATGGAAGAAGAAACTAAGAACAAGAACATGGGGAGGGAG 2375
Db       2044 LysSerLeuAspCysMetHisLysAspGlnValGluLysGluGlyLysValArgGluGlu 2063
Qy       2376 GTCCTCAATCTGACCAAGGAGCTAGAGCTTTCCAAGCGCTACAGCCGAGCTCTCAGGCCG 2435
Db       2064 IleAlaGluTyrGlnLeuArgLeuHisGluAlaGluLysLysHisGlnAlaLeuLeuLeu 2083
Qy       2436 AGTGGGAACGGCCGAAGGATGGTGGACGTGCCTGTGGCCTCCACTGGGGTGCAGACCGAG 2495
Db       2084 AspThrAsnLysGlnTyrGluValGluIleGlnThrTyrArgGluLysLeuThrSerLys 2103
Qy       2496 GCGGTGTGCGGGGATGCTGCGGAGGAGGAGACCCCGGCTGTGTTCATTCGCAAATCCTTC 2555
Db       2104 GluGluCysLeuSerSerGlnLysLeuGlu---------IleAspLeuLeuLysSerSer 2120
Qy       2556 CAGGAGGAA------AATCACATC---------------------------------- 2573
Db       2121 LysGluGluLeuAsnAsnSerLeuLysAlaThrThrGlnIleLeuGluGluLeuLysLys 2140
Qy       2574 ------ATGAGTAATCTTCGACAGGTAGGC---CTGAAGAAACCCATGGAACGGTCC--- 2621
Db       2141 ThrLysMetAspAsnLeuLysTyrValAsnGlnLeuLysLysGluAsnGluArgAlaGln 2160
Qy       2622 TCGGTCCTCGACAGGTATCCCCCAGCAGCGAATGAGCTCACCATGAGGAAGTCTTGGATT 2681
Db       2161 GlyLysMetLysLeuLeuIleLysSerCysLysGlnLeuGluGluGluLysGlu------ 2178
Qy       2682 CCTTGGATGAGAAAAAGAGAAAACGGTCCTTCCACTCCGCAGGAGAAAGGGCCCAGGCCA 2741
Db       2179 ---IleLeuGlnLysGluLeuSerGlnLeuGlnAlaAlaGlnGluLys------------ 2193
Qy       2742 AACCAGGGTGCAGGGCACCCCGGGGAGCTGGTCCTAGCACCAAAGCAGGGCCAGCCCCTA 2801
Db       2194 ------------------------------------------GlnLysThrGlyThrValMet 2200
Qy       2802 CACATCCGTGTG---------ACACCAGATCATGAGAACAGCACTGCCACCCTGGAGATC 2852
Db       2201 AspThrLysValAspGluLeuThrThrGluIleLysGluLeuLysGluThrLeuGluGlu 2220
Qy       2853 ACAAGCCCCACATCTGAAGAGTTTTTCTCTAGT------------------------- 2885
Db       2221 LysThrLysGluAlaAspGluTyrLeuAspLysTyrCysSerLeuLeuIleSerHisGlu 2240
Qy       2886 --------------------------ACCACCGTCATTCCTACCTTAGGCAACCAGAAA 2918
Db       2241 LysLeuGluLysAlaLysGluMetLeuGluThrGlnValAlaHisLeuCysSerGlnGln 2260
Qy       2919 CCAAGAATAACCATTATTCCATCACCCAATGTCATGTCGCAAAAGCCCAAAAGTGCAGAT 2978
Db       2261 ----------------------------------SerLysGlnAspSerArgGlySer 2268
Qy       2979 CCTACTCTCGGCCCAGAACGAGCCATGTCCCCTGTCACGATTACTACTATTTCCAGAGAG 3038
Db       2269 ProLeuLeuGlyProVal---ValProGlyProSerProIleProSerValThrGluLys 2287
Qy       3039 AAGAGCCCGGAAGGTGGAAGGAGCGCCTTTGCCGACAGG---------------------- 3077
```

```
Db       2288 ArgLeuSerSerGlyGlnAsnLysAlaSerGlyLysArgGlnArgSerSerGlyIleTrp 2307
Qy       3078 ----------------------CCTGCATCCCCCATCCAAATCATGACGGTGTCAACATCT 3116
Db       2308 GluAsnGlyGlyGlyProThrProAlaThrProGluSerPheSerLysLysSerLysLys 2327
Qy       3117 GCAGCTCCCACTGAAATCGCTGTCTCTCCTGAATCTCAG------------------- 3155
Db       2328 AlaValMetSerGlyIleHisProAlaGluAspThrGluGlyThrGluPheGluProGlu 2347
Qy       3156 ---------------------------------GAAGTGCCTATGGGAAGGACT------ 3176
Db       2348 GlyLeuProGluValValLysLysGlyPheAlaAspIleProThrGlyLysThrSerPro 2367
Qy       3177 ------ATCCTCAAAGTCACCCCGGAAAAACAAACTGTTCCAGCCCCCGTGCGGAAGTAC 3230
Db       2368 TyrIleLeuArgArgThrThrMetAlaThrArgThrSerProArgLeuAlaAlaGlnLys 2387
Qy       3231 AACTCCAATGCTAATATCATCACCACGGAAGACAATAAAATTCACATTCACCTGGGTTCT 3290
Db       2388 LeuAlaLeuSerProLeuSerLeuGlyLysGluAsn------------------------ 2399
Qy       3291 CAGTTTAAGCGATCTCCTGGGCCTGCCGCTGAAGGCGTGAGCCCAGTTATCACCGTCCGG 3350
Db       2400 ---LeuAlaGluSerSerLysProThrAlaGlyGlySerArgSer-----------Gln 2414
Qy       3351 CCTGTCAACGTGACAGCGGAGAAGGAGGTTTCTACAGGCACAGTCCTTCGCTCTCCCAGG 3410
Db       2415 LysValLysValAlaGlnArgSerProValAspSerGlyThrIleLeuArgGluProThr 2434
Qy       3411 ------------------AACCACCTC---------------------TCTTCAAGACCC 3431
Db       2435 ThrLysSerValProValAsnAsnLeuProGluArgSerProThrAspSerProArgGlu 2454
Qy       3432 GGTGCTAGCAAAGTGACCAGCACTATAACTATAACCCCGGTCACAACGTCATCCACACGA 3491
Db       2455 GlyLeuArgValLysArgGlyArgLeuValProSerProLysAlaGlyLeuGluSerLys 2474
Qy       3492 GGAACCCAATCAGTGTCAGGACAA 3515
Db       2475 GlySerGluAsnCysLysValGln 2482
```

RESULT 5
US-08-353-700-1
; Sequence 1, Application US/08353700
; Patent No. 5599919
; GENERAL INFORMATION:
; APPLICANT: YEN, TIMOTHY J.
; APPLICANT: RATTNER, JEROME B.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING A
; TITLE OF INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DANN, DORFMAN, HERRELL AND SKILLMAN
; STREET: 1601 MARKET STREET, SUITE 720
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,700
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: REED, JANET E.
; REGISTRATION NUMBER: 36,252
; TELECOMMUNICATION INFORMATION:

```
;       TELEPHONE:  (215) 563-4100
;       TELEFAX:  (215) 563-4044
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3248 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     ORIGINAL SOURCE:
;       ORGANISM:  HUMAN
US-08-353-700-1

Alignment Scores:
Pred. No.:                1.17e-21      Length:          3248
Score:                    436.50        Matches:         316
Percent Similarity:       36.27%        Conservative:    240
Best Local Similarity:    20.61%        Mismatches:      527
Query Match:              5.65%         Indels:          450
DB:                       1             Gaps:            63

US-10-788-793-1 (1-4364) x US-08-353-700-1 (1-3248)

Qy          51 TTAAGGAGTCGACAACAGGTGGGAATGAGATCACGAAAT------CAAGGTGGAGAAAGT 104
               |||   ||||||     :::|||:::   :::   :::      ||||||
Db        1746 LeuSerSerArgSerLeuLeuGlyIleAspThrGluAspAlaIleGlnGlyArgAsnGlu 1765

Qy         105 TCA---------TCTAACGGGCATGTCTCCTGCCCCAAGTCCTCCATCATCAGCAGTGAT 155
               |||         |||      |||   |||                          |||
Db        1766 SerCysAspIleSerLysGluHisThrSerGluThrThrGluArgThrProLysHisAsp 1785

Qy         156 GGTGGTAAGGGCCCCTCAGAAGATGCAAAAAAGAACAAGGCCAATCGGAAGGAGGAGGAT 215
                 :::       :::||||||:::::::::      |||          |||
Db        1786 ValHisGlnIleCysAspLysAspAlaGlnGlnAsp---LeuAsnLeuAspIleGluLys 1804

Qy         216 GTCATGGCTTCCGGAACTATCAAAAGGCACCTCAAACCATCTGGAGAA------AGTGAG 269
               :::      :::|||   :::          ||||||:::||||||          |||
Db        1805 IleThrGluThrGlyAlaVal-----------LysProThrGlyGluCysSerGlyGlu 1820

Qy         270 AAAAAGACTAAGAAGTCTGTGGAGTTATCCAAGGAGGACCTCATCCAGCTCCTGAGTATC 329
               :::                :::  |||        ||||||     |||      |||
Db        1821 GlnSerProAspThrAsnTyrGluProProGlyGluAspLysThrGlnGlySerSerGlu 1840

Qy         330 ATGGAAGGGGAGTTGCAG-----------------------------------------GCT 350
                           ||||||
Db        1841 CysIleSerGluLeuSerPheSerGlyProAsnAlaLeuValProMetAspPheLeuGly 1860

Qy         351 CGAGAAGATGTCATCCAC------ATGCTGAGGACAGAGAAAACCAAGCCCGAGGTTCTG 404
                  ::::::   ||||||         ||||||   ::::::|||      |||   |||
Db        1861 AsnGlnGluAspIleHisAsnLeuGlnLeuArgValLysGluThrSerAsnGluAsnLeu 1880

Qy         405 GAG---GCACACTATGGATCTGCAGAACCTGAGAAAGTGCTTCGGGTCCTGCACCGA--- 458
               |||                    ||||||      :::|||:::
Db        1881 ArgLeuLeuHisValIleGluAspArgAspArgLysValGluSerLeuLeuAsnGluMet 1900

Qy         459 ------------------------------------------------------GATGCC 464
                                                                    :::|||
Db        1901 LysGluLeuAspSerLysLeuHisLeuGlnGluValGlnLeuMetThrLysIleGluAla 1920

Qy         465 ATCCTTGCTCAAGAGAAGTCCATAGGAGAAGACGTCTATGAGAAACCTATCTCAGAGCTG 524
                :::      ||||||   :::||||||          :::|||      |||:::|||
Db        1921 CysIleGluLeuGluLysIleValGlyGlu------LeuLysLysGluAsnSerAspLeu 1938

Qy         525 GACAGACTGGAGGAAAAGCAGAAGGAGACGTACCGCCGCATGCTAGAGCAGCTGCTGCTG 584
                    |||                 ::::::   :::|||:::::::::
Db        1939 SerGluLysLeuGluTyrPheSerCysAspHisGlnGluLeuLeuGlnArgValGluThr 1958

Qy         585 GCTGAGAAGTGTCACAGGCGCACCGTGTACGAGCTGGAGAACGAGAAGCACAAGCACACT 644
               :::|||                          |||   ::::::      |||
Db        1959 SerGlu-------,----------------GlyLeuAsnSerAspLeuGluMetHisAla 1970

Qy         645 GACTACATGAACAAGAGCGACGACTTCACCAACCTG---------------------- 680
               |||      ::::::   |||         |||:::
Db        1971 AspLysSerSerArgGluAspIleGlyAspAsnValAlaLysValAsnAspSerTrpLys 1990

Qy         681 --------------CTGGAGCAGGAGCGAGAGAGGTTG---------AAAAAGCTCCTT 716
                           :::|||   |||      |||:::          |||      :::
Db        1991 GluArgPheLeuAspValGluAsnGluLeuSerArgIleArgSerGluLysAlaSerIle 2010

Qy         717 GAACAAGAAAAAGCTTACCAA---------------------------------------- 737
               |||   |||      |||
Db        2011 GluHisGluAlaLeuTyrLeuGluAlaAspLeuGluValValGlnThrGluLysLeuCys 2030

Qy         738 GCCCGCAAAGAAAAGGAAAACGCTAAGCGGCTC------------------------- 770
                  |||:::   ||||||   :::::::::
Db        2031 LeuGluLysAspAsnGluAsnLysGlnLysValIleValCysLeuGluGluGluLeuSer 2050

Qy         771 -----------------AACAAACTTCGAGATGAGCTT------GTGAAGCTCAAGTCC 806
                                |||:::||||||   ||||||      :::      |||:::
Db        2051 ValValThrSerGluArgAsnGlnLeuArgGlyGluLeuAspThrMetSerLysLysThr 2070

Qy         807 TTCGCCCTCATGTTGGTGGACGAGAGGCAG---------------------------- 836
                  ||||||      :::   |||:::
Db        2071 ThrAlaLeuAspGlnLeuSerGluLysMetLysGluLysThrGlnGluLeuGluSerHis 2090

Qy         837 ------------ATGCAC-------------------------------------ATCGAG 848
                           :::|||                                     |||
Db        2091 GlnSerGluCysLeuHisCysIleGlnValAlaGluAlaGluValLysGluLysThrGlu 2110

Qy         849 CAACTGGGCCTGCAGAGTCAGAAAGTCCAGGACCTCACTCAGAAGCTGAGGGAGGAGGAA 908
                  |||          |||      |||   :::|||   :::          :::
Db        2111 LeuLeuGlnThrLeuSerSerAspValSerGluLeuLeuLysAspLysThrHisLeuGln 2130

Qy         909 GAAAAACTCAAAGCGGTCACTTACAAATCCAAGGAAGACCGCCAGAAGCTGCTCAAGTTA 968
               |||||||||:::::::::          :::::::|||   |||   |||
Db        2131 GluLysLeuGlnSerLeu-----------GluLysAspSerGlnAlaLeuSerLeuThr 2146

Qy         969 GAAGTGGACTTCGAACACAAGGCCTCGAGGTTTTCCCAGGAGCACGAAGAGATGAACGCC 1028
               :::   :::   |||:::::::   ::::::   ::::::|||   |||
Db        2147 LysCysGluLeuGluAsnGlnIleAlaGlnLeuAsnLysGluLysGlu----------- 2162

Qy        1029 AAATTGGCGAATCAAGAATCTCACAACCGGCAACTTCGACTCAAA-------------- 1073
                  |||        :::||||||   :::   |||   ||||||
Db        2163 ---LeuLeuValLysGluSerGluSerLeuGlnAlaArgLeuSerGluSerAspTyrGlu 2181

Qy'       1074 ------------------------------------------------------CTGGTT 1079
                                                                      :::
Db        2182 LysLeuAsnValSerLysAlaLeuGluAlaAlaLeuValGluLysGlyGluPheAlaLeu 2201

Qy        1080 GGCTTATCGCAAAGGATTGAGGAGCTGGAAGAGACCAATAAAAGCCTTCAGAAG------ 1133
                  ||||||          ||||||:::   :::      :::   ::::::|||
Db        2202 ArgLeuSerSerThrGlnGluGluValHisGlnLeuArgArgGlyIleGluLysLeuArg 2221

Qy        1134 -----------GCAGAGGAAGAGCTCCAG---GAGCTGAGAGAGAAAATTGCCAAAGGG 1178
                          |||:::|||:::   |||      :::   ||||||:::   :::
Db        2222 ValArgIleGluAlaAspGluLysLysGlnLeuHisIleAlaGluLysLeuLysGluArg 2241

Qy        1179 GAATGTGGAAACTCCAGTCTCATGGCGGAAGTGGAGAGTCTGCGCAAGCGC--------- 1229
               |||      |||   ||||||      :::||||||:::|||   :::
Db        2242 GluArgGluAsnAspSerLeuLysAspLysValGluAsnLeuGluArgGluLeuGlnMet 2261

Qy        1230 ------------------------GTGCTTGAGATGGAGGGCAAGGATGAAGAGATCACG 1265
                                      :::|||:::   |||            |||:::
Db        2262 SerGluGluAsnGlnGluLeuValIleLeuAspAlaGluAsnSerLysAlaGluValGlu 2281

Qy        1266 AAGACCGAGGCCCAGTGCCGGGAGCTGAAGAAGAAGCTCCAAGAGGAAGAACACCACAGC 1325
                  :::   |||      |||:::   :::   |||:::      |||
Db        2282 ThrLeuLysThrGlnIleGluGluMetAlaArgSerLeuLysIlePheGluLeuAspLeu 2301

Qy        1326 AAGGAACTTAGACTAGAAGTGGAGAAGCTGCAGAAG--------------------AGG 1364
                  ||||||   |||   |||   |||   |||                      :::
Db        2302 ValThrLeuArgSerGluLysGluAsnLeuThrLysGlnIleGlnGluLysGlnGlyGln 2321

Qy        1365 ATGTCTGAGCTGGAGAAGCTGGAGGAAGCGTTCAGCCGGAGTAAGTCGGAATGCACCCAG 1424
```

```
Db      2322 LeuSerGluLeuAspLysLeuLeuSerSerPheLysSerLeuLeuGluGluLysGluGln 2341
Qy      1425 CTCCATCTGAACCTGGAGAAGGAGAAGAACCTAACCAAAGACCTGCTG---AACGAGCTG 1481
Db      2342 AlaGluIleGlnIleLysGluGluSerLysThrAlaValGluMetLeuGlnAsnGlnLeu 2361
Qy      1482 GAGGTGGTCAAGAGTCGAGTTAAAGAACTCGAATGCTCCGAGAGTAGACTGGAGAAGGCC 1541
Db      2362 LysGluLeuAsnGluAlaValAlaAlaLeu---CysGlyAspGlnGluIleMetLysAla 2380
Qy      1542 --------------------------------GAGTTAAGCCTCAAAGATGACCTTACA 1568
Db      2381 ThrGluGlnSerLeuAspProProIleGluGluGluHisGlnLeuArgAsnSerIleGlu 2400
Qy      1569 AAGCTGAAGTCCTTCACTGTGATGCTGGTGGATGAGAGGAAAAATATG------ATGGAG 1622
Db      2401 LysLeuArgAla------ArgLeuGluAlaAspGluLysLysGlnLeuCysValLeuGln 2418
Qy      1623 AAAATAAAGCAAGAAGAGAGGAAAGTGGATGGGTTGAATAAAAACTTTAAGGTGGAGCAG 1682
Db      2419 GlnLeuLysGluSerGluHisHisAlaAspLeuLeu--------------------Lys 2431
Qy      1683 GGAAAAGTCATGGATGTGACGGAAAAGCTA---------------------------- 1712
Db      2432 GlyArgValGluAsnLeuGluArgGluLeuGluIleAlaArgThrAsnGlnGluHisAla 2451
Qy      1713 ---------ATCGAGGAAAGCAAG---------AAGCTTTTAAAACTCAAATCTGAA--- 1751
Db      2452 AlaLeuGluAlaGluAsnSerLysGlyGluValGluThrLeuLysAlaLysIleGluGly 2471
Qy      1752 --------------------ATGGAGGAAAAGGAGTACAGTCTGACAAAGGAGAGGGAT 1790
Db      2472 MetThrGlnSerLeuArgGlyLeuGluLeuAspValValThrIleArgSerGluLysGlu 2491
Qy      1791 GAGCTGATGGGTAAACTGAGGAGCGAAGAAGAAAGGTCCTGTGAACTG----------- 1838
Db      2492 AsnLeuThrAsnGluLeuGlnLysGluGlnGluArgIleSerGluLeuGluIleIleAsn 2511
Qy      1838 ------------------------------------------------------------ 1838
Db      2512 SerSerPheGluAsnIleLeuGlnGluLysGluGlnGluLysValGlnMetLysGluLys 2531
Qy      1839 ---AGCTGCAGTGTAGACTTACTAAAGAAGCGGCTTGATGGCATA---GAGGAGGTAGAA 1892
Db      2532 SerSerThrAlaMetGluMetLeuGlnThrGlnLeuLysGluLeuAsnGluArgValAla 2551
Qy      1893 AGGGAAATAAACCGAGGTAGGTCGTGCAAG----------------GGGTCTGAGTTC 1934
Db      2552 AlaLeuHisAsnAspGlnGluAlaCysLysAlaLysGluGlnAsnLeuSerSerGlnVal 2571
Qy      1935 ACCTGCCCGGAA---------------------------------------------- 1946
Db      2572 GluCysLeuGluLeuGluLysAlaGlnLeuLeuGlnGlyLeuAspGluAlaLysAsnAsn 2591
Qy      1947 ----------------------------------------------GACAAT 1952
Db      2592 TyrIleValLeuGlnSerSerValLysGlyLeuIleGlnGluValGluAspGlyLysGln 2611
Qy      1953 AAGATCAGAGAACTAACGCTTGAAATCGAGAGACTGAAGAAACGGCTCCAGCAGTTGGAG 2012
Db      2612 LysLeuGluLysLysAspGluGluIleSerArgLeuLysAsnGlnIleGlnAspGlnGlu 2631
Qy      2013 GTGGTGGAGGGGGACTTGATGAAGACCGAGGACGAATATGAC----------------- 2054
Db      2632 GlnLeuValSerLysLeuSerGlnValGluGlyGluHisGlnLeuTrpLysGluGlnAsn 2651
Qy      2055 ----------------------CAGTTGGAGCAGAAGTTCAGAACCGAGCAGGATAAG 2090
Db      2652 LeuGluLeuArgAsnLeuThrValGluLeuGluGlnLysIleGlnValLeuGlnSerLys 2671
Qy      2091 GCAAACTTCCTCTCCCAGCAGCTCGAGGAAATCAAACAC------------------- 2129
```

```
Db      2672 AsnAlaSerLeuGlnAspThrLeuGluValLeuGlnSerSerTyrLysAsnLeuGluAsn 2691
Qy      2130 --------------CAAATGGCCAAGCACAAAGCCATAGAGAAA---GGGGAGGCCGTG 2171
Db      2692 GluLeuGluLeuThrLysMetAspLysMetSerPheValGluLysValAsnLysMetThr 2711
Qy      2172 AGCCAGGAAGCCGAACTGCGACACAGGTTTCGGCTGGAGGAGGCTAAAAGTCGTGATTTA 2231
Db      2712 AlaLysGluThrGluLeuGlnArgGluMetHisGluMetAlaGlnLysThrAlaGluLeu 2731
Qy      2232 CAGGCCGAGGTGCAGGCTCTCAAGGAGAAG----------------------ATCCAC 2267
Db      2732 GlnGluGluLeuSerGlyGluLysAsnArgLeuAlaGlyGluLeuGlnLeuLeuGluLeu 2751
Qy      2268 GAGCTGATGAACAAGGAAGACCAGCTGTCTCAGCTCCAAGTCGACTATTCGGTCCTTCAG 2327
Db      2752 GluIleLysSerSerLysAspGlnLeuLysGluLeuThrLeuGluAsnSerGluLeuLys 2771
Qy      2328 CAAAGATTT-----------ATGGAAGAAGAAACTAAGAACAAGAACATGGGGAGGGAG 2375
Db      2772 LysSerLeuAspCysMetHisLysAspGlnValGluLysGluGlyLysValArgGluGlu 2791
Qy      2376 GTCCTCAATCTGACCAAGGAGCTAGAGCTTTCCAAGCGCTACAGCCGAGCTCTCAGGCCG 2435
Db      2792 IleAlaGluTyrGlnLeuArgLeuHisGluAlaGluLysLysHisGlnAlaLeuLeuLeu 2811
Qy      2436 AGTGGGAACGGCCGAAGGATGGTGGACGTGCCTGTGGCCTCCACTGGGGTGCAGACCGAG 2495
Db      2812 AspThrAsnLysGlnTyrGluValGluIleGlnThrTyrArgGluLysLeuThrSerLys 2831
Qy      2496 GCGGTGTGCGGGGATGCTGCGGAGGAGGAGACCCCGGCTGTGTTCATTCGCAAATCCTTC 2555
Db      2832 GluGluCysLeuSerSerGlnLysLeuGlu---------IleAspLeuLeuLysSerSer 2848
Qy      2556 CAGGAGGAA------AATCACATC---------------------------------- 2573
Db      2849 LysGluGluLeuAsnAsnSerLeuLysAlaThrThrGlnIleLeuGluGluLeuLysLys 2868
Qy      2574 ------ATGAGTAATCTTCGACAGGTAGGC---CTGAAGAAACCCATGGAACGGTCC--- 2621
Db      2869 ThrLysMetAspAsnLeuLysTyrValAsnGlnLeuLysLysGluAsnGluArgAlaGln 2888
Qy      2622 TCGGTCCTCGACAGGTATCCCCCAGCAGCGAATGAGCTCACCATGAGGAAGTCTTGGATT 2681
Db      2889 GlyLysMetLysLeuLeuIleLysSerCysLysGlnLeuGluGluGluLysGlu------ 2906
Qy      2682 CCTTGGATGAGAAAAAGAGAAAACGGTCCTTCCACTCCGCAGGAGAAAGGGCCCAGGCCA 2741
Db      2907 ---IleLeuGlnLysGluLeuSerGlnLeuGlnAlaAlaGlnGluLys------------ 2921
Qy      2742 AACCAGGGTGCAGGGCACCCCGGGGAGCTGGTCCTAGCACCAAAGCAGGGCCAGCCCCTA 2801
Db      2922 ------------------------------------GlnLysThrGlyThrValMet 2928
Qy      2802 CACATCCGTGTG---------ACACCAGATCATGAGAACAGCACTGCCACCCTGGAGATC 2852
Db      2929 AspThrLysValAspGluLeuThrThrGluIleLysGluLeuLysGluThrLeuGluGlu 2948
Qy      2853 ACAAGCCCCACATCTGAAGAGTTTTTCTCTAGT------------------------- 2885
Db      2949 LysThrLysGluAlaAspGluTyrLeuAspLysTyrCysSerLeuLeuIleSerHisGlu 2968
Qy      2886 --------------------------ACCACCGTCATTCCTACCTTAGGCAACCAGAAA 2918
Db      2969 LysLeuGluLysAlaLysGluMetLeuGluThrGlnValAlaHisLeuCysSerGlnGln 2988
Qy      2919 CCAAGAATAACCATTATTCCATCACCCAATGTCATGTCGCAAAAGCCCAAAAGTGCAGAT 2978
Db      2989 ------------------------------------SerLysGlnAspSerArgGlySer 2996
Qy      2979 CCTACTCTCGGCCCA---GAACGAGCCATGTCCCCTGTCACGATTACTACTATTTCCAGA 3035
Db      2997 ProLeuLeuGlyProValValProGlyProSerProIleProSerValThrGluLysArg 3016
```

```
Qy       3036 GAGAAGAGCCCGGAAGGTGGAAGGAGCGCCTTTGCCGACAGGCCTGCATCCCCCATCCAA 3095
Db       3017 LeuSerSerGlyGlnAsnLysAlaSerGlyLysArgGlnArgSerSerGlyIleTrpGlu 3036
Qy       3096 ATCATGACGGTGTCAACATCTGCAGCTCCCACTGAAATCGCTGTCTCTCCTGAATCTCAG 3155
Db       3037 AsnGlyArgGlyProThrProAlaThrProGlu------SerPheSerLysLysSer-Ly 3054
Qy       3156 GAAGTGCCTATGGGAAGGACTATCCTCAAAGTCACCCCGGAAAAACAAACTGTTCCAGCC 3215
Db       3054 sLysAlaValMetSerGlyIleHisProAlaGluAspThrGluGlyThrGluPheGluPr 3074
Qy       3216 C----------------------------------------CCGTGCGGAAGTACAAC 3233
Db       3074 oGluGlyLeuProGluValValLysLysGlyPheAlaAspIleProThrGlyLysThrSe 3094
Qy       3234 TCCAATGCTAATATCATCACCACGGAAGACAATAAAATTCACATTCACC---------- 3282
Db       3094 rProTyrIleLeu---------ArgArgThrThrMetAlaThrArgThrSerProArgLe 3111
Qy       3283 -------TGGGTTCTCAGTTTAAGCGATCTC---CTGGGCCTGCCGCTGAAGGCGTGAGC 3332
Db       3111 uAlaAlaGlnLysLeuAlaLeuSerProLeuSerLeuGlyLysGluAsnLeuAlaGluSe 3131
Qy       3333 CCAGTTATCACCGTCCGGCCTGTCAACGTGACAGCGGAGAAGGAGGTTTCTACAGGCACA 3392
Db       3131 rSerLysProThrAlaGlyGlySer---------ArgSerGlnLysValLysValAlaGl 3148
Qy       3393 GTCCTTCGCTCTCCCAGGAACCACCTCTCTTCAAGACCCGGTGCTAGCAAAGTGACCAGC 3452
Db       3148 nArgSerProValAspSerGlyThrIleLeuArgGluProThrThrLysSerValProVa 3168
Qy       3453 ACTATAACTATAACCCCGGTCACAACGTCATCCACACGAGGAACCCAATCAG---TGTCA 3509
Db       3168 lAsnAsnLeu---------ProGluArgSerProThrAspSerProArgGluGlyLeuAr 3185
Qy       3510 GGACAAGATGGGTCATCTCAGCGGCCTACCCCCACCC 3546
Db       3185 gValLysArgGlyArgLeu------ValProAlaPro 3195
```

RESULT 6
PCT-US95-16216-1
; Sequence 1, Application PC/TUS9516216
; GENERAL INFORMATION:
; APPLICANT: Yen, Timothy J.
; APPLICANT: Rattner, Jerome B.
; TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
; TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods of Use
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16216
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/353,700
; FILING DATE: 09-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3248 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US95-16216-1

Alignment Scores:

Pred. No.:			
Score:	1.17e-21	Length:	3248
Percent Similarity:	436.50	Matches:	316
Best Local Similarity:	36.27%	Conservative:	240
Query Match:	20.61%	Mismatches:	527
DB:	5.65%	Indels:	450
	5	Gaps:	63

US-10-788-793-1 (1-4364) x PCT-US95-16216-1 (1-3248)

```
Qy         51 TTAAGGAGTCGACAACAGGTGGGAATGAGATCACGAAAT------CAAGGTGGAGAAAGT 104
Db       1746 LeuSerSerArgSerLeuLeuGlyIleAspThrGluAspAlaIleGlnGlyArgAsnGlu 1765
Qy        105 TCA---------TCTAACGGGCATGTCTCCTGCCCCAAGTCCTCCATCATCAGCAGTGAT 155
Db       1766 SerCysAspIleSerLysGluHisThrSerGluThrThrGluArgThrProLysHisAsp 1785
Qy        156 GGTGGTAAGGGCCCCTCAGAAGATGCAAAAAAGAACAAGGCCAATCGGAAGGAGGAGGAT 215
Db       1786 ValHisGlnIleCysAspLysAspAlaGlnGlnAsp---LeuAsnLeuAspIleGluLys 1804
Qy        216 GTCATGGCTTCCGGAACTATCAAAAGGCACCTCAAACCATCTGGAGAA------AGTGAG 269
Db       1805 IleThrGluThrGlyAlaVal----------LysProThrGlyGluCysSerGlyGlu 1820
Qy        270 AAAAAGACTAAGAAGTCTGTGGAGTTATCCAAGGAGGACCTCATCCAGCTCCTGAGTATC 329
Db       1821 GlnSerProAspThrAsnTyrGluProProGlyGluAspLysThrGlnGlySerSerGlu 1840
Qy        330 ATGGAAGGGGAGTTGCAG----------------------------------------GCT 350
Db       1841 CysIleSerGluLeuSerPheSerGlyProAsnAlaLeuValProMetAspPheLeuGly 1860
Qy        351 CGAGAAGATGTCATCCAC------ATGCTGAGGACAGAGAAAACCAAGCCCGAGGTTCTG 404
Db       1861 AsnGlnGluAspIleHisAsnLeuGlnLeuArgValLysGluThrSerAsnGluAsnLeu 1880
Qy        405 GAG---GCACACTATGGATCTGCAGAACCTGAGAAAGTGCTTCGGGTCCTGCACCGA--- 458
Db       1881 ArgLeuLeuHisValIleGluAspArgAspArgLysValGluSerLeuLeuAsnGluMet 1900
Qy        459 ----------------------------------------------------------GATGCC 464
Db       1901 LysGluLeuAspSerLysLeuHisLeuGlnGluValGlnLeuMetThrLysIleGluAla 1920
Qy        465 ATCCTTGCTCAAGAGAAGTCCATAGGAGAAGACGTCTATGAGAAACCTATCTCAGAGCTG 524
Db       1921 CysIleGluLeuGluLysIleValGlyGlu------LeuLysLysGluAsnSerAspLeu 1938
Qy        525 GACAGACTGGAGGAAAAGCAGAAGGAGACGTACCGCCGCATGCTAGAGCAGCTGCTGCTG 584
Db       1939 SerGluLysLeuGluTyrPheSerCysAspHisGlnGluLeuLeuGlnArgValGluThr 1958
Qy        585 GCTGAGAAGTGTCACAGGCGCACCGTGTACGAGCTGGAGAACGAGAAGCACAAGCACACT 644
Db       1959 SerGlu----------------------GlyLeuAsnSerAspLeuGluMetH
Qy        645 GACTACATC
```